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AL066286 Drosophil
BX416727 BX416727
BX436369 BX436369
AG127412 Pan trogl
                                                                                                October 29, 2003, 21:18:11; Search time 2502.29 Seconds (without alignments) 8935.871 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                              22781392 segs, 12152238056 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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| CNSO073W CNSO04ENY AL581979 AQ743305 CNSO0FXE CNSO0FXE CNSO0FXE CNSO01224 CNSO10224 CNSO10224 CNSO10224 AQ128925 AQ128929 AQ139490 CNSO117M AQ128016 AQ743349 AQ128016 AQ743349 AQ128017 AQ139490 CNSO117M AG128017 AG128017 AG128017 AG128019 AG128019 AG128018 AG128019 AG127518 AG128019 AG128019 AG128019 AG128019 AG128019 AG127518 AG128019 AG128019 AG128019 AG128019 AG128019 AG1277433 AG12 | |
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Pull-length cDNA libraries and normalization Unpublished
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 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCOI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 712)

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13.0%; Score 120; DB 29; Length 8
Best Local Similarity 25.0%; Pred. No. 4.3e-10;
Matches 129; Conservative 186; Mismatches 201; Indels
                                                                                                                                                         /organism="Drogophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/note="end : TET3"
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/wol type="maxNa"
/db_xref="taxon:9606"
/dlone="csopally114"
/tissue_type="NEKROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
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8X436369 Homo sapiens THYMUS Homo sapiens CDNA clone CSOCAP001YM12
5-PRIME, mRNA sequence.
BX436369
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1180)
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Ferry Liang Email : fliangelifetech.com Uhttp://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODA011BE07QP1.
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Best Local Similarity 14.1%; Pred. No. 6.1e-09;
Matches 57; Conservative 221; Mismatches 127; Indels
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                       GSS 04-NOV-2001
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                                                                                                                                             27412
troglodytes DNA, clone: PTB-138E06.R, genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/clone_lib="PTB Chimpanzee Male BAC Library"
351 c 31 g 23 t 36 others
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="PTB-138E06.R"
                                                                                                                                                                                                                                                                            Pan troglodytes (chimpanzee)
Pan troglodytes
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                  612 AAAAAGHYYNTKHHYTYY 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"

/mol_type="mRNA"

/db_txfe="txxx01:9606"

/dlone="CSOCAPO01YM12"

/tissue_type="THYMU2"

/tissue_type="THYMU2"

/clone="type="THYMU2"

/clone="type="THYMU2"

/note="type="THYMU2"

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BP 191 91006 EVRY cedex - France
BRail: seqrefégenoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 516.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSOCAP001BG06Qpl&cluster=516.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001BG06Qpl.
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                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Craracterization and repeat analysis of the compact genome of freshwater pufferish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
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                                                                                                                                  102; Conservative 164; Mismatches 144; Indels
                                                                             DB 29;
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                                                                         11.2%; Score 103.2; 24.8%; Pred. No. 2.3
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Tetraodon nigroviridis
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Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Droscophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BACs. For further information please see http://www.frnifiy.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutcyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of broscophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

Location/Qualifiers
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
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/fissue type="B CELIS (RAMOS CELL LINE)"
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       Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cacdx - France
BRail: 991 91006 EVRY cacdx - France
BRail: seqref@genoscope.cms.fr, Www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8262.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-blin/cluster.cgi?seq=CSODG004CC08NPI&cluster=8262.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODG004CC08NPI.
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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
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CELLS (RAMOS CELL LINE) Homo sapiens cDNA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                   sequence ID : COBG104DH07LP1~end : T7"
g 409 t 71 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AAATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744 CACTGCTCACCAACAACACACCAAGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCC
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                                                                                                                                                                                                                                                                                                                               71 others
                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 101.8; DB 29; Length
46.0%; Pred. No. 3.8e-07;
.ive 36; Mismatches 222; Indels
                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="104P14"
/clone lib="G"
/note="Genoscope sequence ID : C0BG1
a 86 c 254 g 409 t 71 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL581589 Homo sapiens B CELLS FRAMOS CELL
Clone CSODGO04YF15 3-PRIME, mRNA sequence.
AL581589 GI:12948741
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es 227; Conser
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TITLE
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SOURCE
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                            COMMENT
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/Glone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

301 c 16 g 15 t 49 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 16-JUL-1999
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;
                                                                                                                                                                                                                Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clonea are derived from the human BAC library RPCI-11. For BAC
Clonea are derived from the contact Pieter de Jong
(pieter@dejong.med.buffalo.edu, Clonea may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1141)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                             806 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
746 CTGCTCACCAACAACACCACAGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS 5387 B2 B02 SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=963 Col=4 Row=D, genomic survey sequence.
                                                                                                                                                                                                                                                                                                     721 cdgcccccccccccccccrrtttttttttttiiiii
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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Pred. No. 9.1e-07;
0; Mismatches 425;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=963 Col=4 Row=D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.htsc.washington.edu
Plate: 963 row: D column: 4
Seg primer: SP6
Class: BAC ends
High quality sequence stop: 1141.
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Best Local Similarity 46.3%;
Matches 370; Conservative (
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                                                                                  EST 23-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODW003CB02QP1&cluster=8045.f. Contact :
Feng Liang Email : fliangedlifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen.com/ Email Sanday Avenue Genoscope sequence ID : CSODW003CB02QP1.
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1 (Seas 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8045.f For
more information about this cluster, see
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                                                                           AL531977
AL531977 Homo sapiens FETAL LIVER Homo sapiens CDNA clone CSODW003YD03 5-PRIME, MENA sequence.
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KEYWORDS
SOURCE
ORGANISM
            RESULT 8
AL531977/c
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AUTHORS
TITLE
JOURNAL
COMMENT
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Web: www.genoscope.cns.fr/loans.cs.genoscope.cns.fr/loans.cs.genoscope.cns.fr/loans.cs.genoscope.cns.fr/loans.cs.genoscope.cns.fr/loans.cs.genoscope.cns.fr/loans.cs.genoscope.genoscope.cns.genome using these BACs.end Genome Project (BDCP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutcyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named REC1.98 and was constructed by partial BCOMI digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2; cn bw sp, the same strain used for the BDCP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be located that it is in the control of the backer can be located by conditions.come individual filers
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1081 AAAMACMMMARAMACMWACAMMACAMMCCMWCMWAWAMMMACAGMFINCKKOMMCM 1022
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                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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10.8%; Score 99; DB 29; Length 11
Best Local Similarity 25.6%; Pred. No. 1.1e-06;
Matches 104; Conservative 145; Mismatches 157; Indels
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Gasterosteus aculeatus

    .1101
/organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"

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/clone_lib="RPCI-98"
/note="end : TET3"
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR32C19 of RPCI-98 library from Drosophila melanogaster (fruit
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CAAATCACATTATCCATTCTGGCAATGATAATCTCCAACTTCACTTATAATTACAGCCATC 184
                                                   680 APACRARARARCARCCARCARARARCACRARARCACCCCARARARARARARARA 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603 CCACCAAGCCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAA 662
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                                                                                                            ATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA--TG
                                                                                                                                                             363 CACCAGGAGTCAAGTCAAACCTGCAACCACAACAGTCAAGACTAAAAAACACAAAAA
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Meoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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S Li,W B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length CDNA libraries and normalization
Ompublished
On Feb 15, 2001 this sequence version replaced gi:12882945.
On Feb 15, 2001 this sequence version replaced gi:12882945.
On Feb 15, 2001 this sequence version replaced gi:12882945.
Contact: Genoscope
Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 113.r For more information about this cluster, see thtp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1034BCO10P1&cluster=113.r. Contact: Feng Liang Email: flianglifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1034BC010F1.
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AL548181 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSODI034YE02 5-PRIME, mRNA sequence.
AL548181
                                                                                                                                                                                                                                                                857
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Not1-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 362 c 185 g 95 t 111 others
        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
                                                                                                        618 AAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGG
                                                                                                                                                                                                           798 CCTTCCACTCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACACATCCG
                                                          558 CINICIGCANANGANIACCANACANANANCCAGGANAGANANCCACCACCACCAGCCIACAN
                                                                                                                                                                                                                                                                                                                                                                   738 CAACTACACTCACCAACACACACACAGGAAATCCAAAACTCACAAGTCAAATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                      9; Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           858 AGCACCCATCACAACCCTCATCTCCACCCAACAACA 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 CCCCCCCCCCNNCNNNCCCCNCCAAAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 97.2; DB Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1034YE02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Best Local Similarity
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ORGANISM
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AL548181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / GEORGE "CLAMBE TOU."
/ FISSUE_TYDE="LAGE and female"
/ tissue_type="heads and internal organs combined"
/ dev stage="adult"
/ clone_lib="SHGC-CDA"
/ clone_lib="SHGC-CDA"
/ note="Vector: lambda ZAP Express/DBK-CMV; Site_1: EcoRl
/ note="Vector: lambda ZAP Express/DBK-CMV; Site_1: EcoRl
(5' adaptor); Site_2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a a 50 bp linker primer containing an oligo dT sequence
preceeded by a synthetic XhoI site. 5 prime adaptors were
used containing an EcoRl cohesive end. The finished cDNAs
were inserted in to the ZAP express vector.
unidirectionally in the sense orientation with respect to
the lacZ promoter of pRW-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
                                                                                                                                                                                                                             Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
Tel: 650 725 5954
Fax: 650 725 7739
Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gasterosteidae, Gasterosteus.

1 (bases 1 to 1151)

1 (bases 1 to 1151)

1 (schugley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.

Expressed sequence tags from Gasterosteus aculeatus

Unpublished
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAACCCCAACATACCTCAGGATCCTCAGCTTGGAATCAGCTTCTCCAATCTGTC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACCACAAAAGTCACACTAACAACTGCAATCATACAAGATGCAAAAAGATCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 TGAAATTACATC----ACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 CAAACCIGCAACCCACAAAAGICAAGACIAAAAACACAACAACAACAACAACAACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 98; DB 14; Length 1151; 45.7%; Pred. No. 1.5e-06; ive 0; Mismatches 375; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gasterosteus aculeatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="Salinas river, CA"
/db_xref="taxon:69293"
/clone="CDA48-F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 3
High quality sequence stop: 263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Best Local Similarity 45.77
Matches 319, Conservative
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                                                                                                                                                                           TITLE
JOURNAL
COMMENT
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                                                                                                        REFERENCE
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155 AICTCAACTICACTTATAATTACAGCCATCATATTCATAGCCTCGGCAAACCACAAGTC 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 AACAAAACCCCACAACCCAAAACCCACAACCCCCACTCCCCACAAAACAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 ACAGTCAAGACTAAAAACACAAAAAACCAAAACACAAAGCCCAGGAAGCCCACTACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTITIGIACCCIGCAGCATAIGCAGCAACAATCCAACCTGCTGGGCTAICTGCAAAAGAA
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                                                                                                                                                                                                                                                                                                                               Length 1024;
                                                                                                                                                                                                                                                                 Chimpanzee Male BAC Library
                                                                                                                                                                                                                                                                                   others
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                            Score 96.6; DB 29;
Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 390;
                                                                                                                                               1..1024
/organism="Pan troglodytes"
/mol type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-145K08.R"
                                                                                                                                                                                                                                                                                40 t
                                                                                                                                                                                                                             /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanze
460 c 23 g 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               873 CCTCATCTCCACCCAACACACACGCCA 900
                                                                                                                                  Location/Qualifiers
        was generated during the clone tracking errors.
                                                                                     : pKS145
                                                      Sequencing: M13Rev
                                                                                    Vector : pKS1
R.Site 1 : SacI
R.Site 2 : SacI
                                                                                                                                                                                                                                                                                                                            Query Match
10.5%;
Best Local Similarity 47.3%;
Matches 354; Conservative
                                     PRIMERS
                                                                   LIBRARY
                                                                                                                                                                                                                                                                              495
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Best Local
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Pax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG133080 1024 bp DNA linear GSS 04-NOV-2001
Pan troglodytes DNA, clone: PTB-145K08.R, genomic survey sequence.
AG133080
                                                           CATACAAGATGCAACAAGCCAGATCAAGAACACAACCCCCAACATACCTCACGCACCTCAGGATCC 291
                                                                                                                     TCAGCTTGGAATCAGCTTCTCCAATCTGTGAAATTACATCACAAACCACCATACT 351
                                                                                                                                                                             CACAACAACAACCCA-----AACACCAAGCCAGCAAGCCCACTACAAAACAAGGCCAAAA 464
                                                                                                                                                                                                                                                                                                                         872
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                                                                                                                                                                                                                                                                                                                                                                                                                       576
                                                                                                                                                                                                                                          AGCTTCAACAACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAA 411
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                     172 AATTACAGCCATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAAT
                                                                                                                                                                                                                                                                                                                                                   -----ACAAACCACCAAACAAACCAATAATGATTTTCACTTCGAAGTGTTTAACTT
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      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1024)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T. Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
   82; Mismatches 279; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 CACAAMCAAACCCAACAAAACCAAMAMM 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACACCACAGGAAATCCAAAACTCACA 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG133080.1 GI:16662758
252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                            232
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                                                                                                                                                                                                                                                                                      412
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AUTHORS
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SOURCE
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261

334

381

394

454 501 512

561

572

621

632

681 692 741 752

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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr / Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4073.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSODL006BC06NPl&cluster=4073.r. Contact :
Feng Liang Bail: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODL006BC06NPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX385076

BX385076 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED HOMO sapiens cDNA clone CSODL006YE12 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                    13 MMANACMMWAAACCCCMM ---MAAACCAMMMCCCMCCCMMCCCCCMMANCCCCCCCCAMMCC 157
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the PCMVSPORT 6 vector. Library was normalized.
I75 c 126 g 196 t 170 others
                                                                                                                                                                                                                                                                                                                                           AGAAAACCACCACCAACCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAAGATCTCA
                                                                                                                                                                                                           714 TCAACACCACCAAAACAAACATCACAACTACACTGCTCACCAACAACACCACAGGAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        774 CAAAACTCACAAGTCAAATGGAAACCTTCCACTCAACCTCCTCCGAAGGCAATCTAAGCC
                                                                                                                                                                                                                                                                         654 AACCICAAACCACIAAACCAAAGGAAGIACCCACCACCAAGCCCACAGAAGAGCCAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               834 CTICTCAAGTCTCCACAACATCCGAGCACCCATCACAACCCTC 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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Best Local Similarity 38.93
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/note="Vector: pCMYSPORT 6; lat strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
138 a 29 c 99 g 264 t 308 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 AGCTTGGAATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Livitrogen. This sequence belongs to sequence cluster 3806.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODH001DC02NP1&cluster=3806.r. Contact :
Feng Liang Email : fliangelifecch.com VEL :
http://fulllength.invitrogen.com/ luyitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODH001DC02NP1.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea I to 753)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                                                                                                                                                                                      753 bp mRNA BX443342 Homo sapiens T CELLS (JURKAT CELL Clone CSODHOO1YF04 3-PRIME, mRNA sequence. BX443342
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                     sapiens (human)
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Best Local
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972 MWANMCCAMACCMBAAAACCMAABAAACAAMBAACCAABAAAACCCCAMBAAMMACA 1031
                            351 INGCTTCAACAACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAA 410
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                                                                                            591 GAAAGAAAACCACCACCAAGCCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAATC 650
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Search completed: October 30, 2003, 01:15:23 Job time : 2507.29 secs us-09-462-816-1.rnpb

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LENGTH: 15223 base pairs
TYPE: nucleic acid
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US-09-847-173-1
76.6
76.4
76.4
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75.2
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7.00.6
4.00.7
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Sequence 10, Appl
Sequence 1076, Ap
Sequence 4304, Ap
Sequence 2, Appli
Sequence 1981, Ap
Sequence 1981, Ap
Sequence 378, Appl
Sequence 378, Appl
Sequence 20, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1670, Ap
Sequence 20241, Ap
Sequence 3471, Ap
Sequence 20536, A
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                                                                                     October 30, 2003, 00:01:13; Search time 310.043 Seconds (without alignments) 8070.528 Million cell updates/sec
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                                                                                                                                             US-09-462-816-1
920
1 tgcaaacatgtccaaaaaca.....gtagttattaaaaaaaaa 920
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                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*

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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-311-455-1076

0 US-09-878-574-4304

12 US-10-312-841-2

2 US-10-017-161-1981

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2 US-10-311-455-378

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2 US-10-240-455-37

4 US-10-239-676-12

2 US-10-239-676-12

2 US-10-239-676-12

2 US-10-239-676-12

US-09-864-761-2471

US-09-864-761-3471
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                                                                                                                                                                                                                                               1811591 seqs, 1359896290 residues
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                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                    Scoring table:
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637.4
441.4
86.2
85.8
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                                                                                         Run on:
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Sequence 4296, Ap Sequence 2109, Ap Sequence 19241, A Sequence 19241, A Sequence 19213, Ap Sequence 675, App Sequence 675, App Sequence 1931, Ap Sequence 25133, A Sequence 25133, A Sequence 1241, Ap Sequence 1241, Ap Sequence 1871, App Sequence 1857, App Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Appli
Sequence 1793, Ap
Sequence 45, Appl
Sequence 401, App
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Sequence 1, Application US20020182228A1
GENERAL INFORMATION:
GENERAL THORMATION:
APPLICANT: Collins, Peter L.
TITLE OF INVENTION: PRODUCTION OF INFECTIOUS RESPIRATORY
SYNCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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SURTEX: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/847,173
FILING DATE: 03-May-2001
FILING DATE: 04-May-2001
FILING DATE: 04-May-2001
FILING DATE: 4UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/720,132
ATTORNEY/AGENT INFORMATION:
NAME: PATTNESS: 21.990
REFERENCS/DOCKET NUMBER: 15.280-250-1
TELLEGOMUNICATION:
MEPRENCS/DOCKET NUMBER: 15.280-250-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
10 US-09-878-574-4296
10 US-09-818-574-4296
10 US-09-818-574-4296
10 US-09-864-761-19241
12 US-10-311-455-1669
12 US-09-864-761-2513
12 US-10-311-455-675
12 US-10-311-455-675
12 US-10-311-455-675
12 US-10-311-455-1291
12 US-10-029-386-22723
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12 US-10-311-455-1783
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12 US-10-240-485-45
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TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 1:
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RESULT 2
US-09-844-645-4
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                                                                            DB 10, Length 15223;
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                                                                                                    Indels
                                                                           Query Match 92.8%; Score 853.4; DB 10; Best Local Similarity 95.5%; Pred. No. 1.8e-210; Matches 878; Conservative 0; Mismatches 41;
                           SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-847-173-1
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STRANDEDNESS: single
              TOPOLOGY: linear
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Pred. No. 3.7e-155;
0; Mismatches 26; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                            APPLICANT: Briles, David E.
McDaniel, Larry S.
Curiel, David T.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR ADMINISTERING PNEUMOCCCCAL
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford,
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2450
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 840-3333
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,505
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,645
FILING DATE: 27-Apr-2001
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECTLE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-844-645-4
Sequence 4, Application US/09844645
Patent No. US20020102242A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 96.1%;
Matches 664; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                  NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: U.S.A.
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Diseases Associated with the Immune System by Dete
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         1923 AATAAAAACCACACTGAAAAAACATCACCACCTACCTTACTCAAGTCCCCACCAGAAAG 4982
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                                                                                                5043 Arcaccarcaaagrcagaaacacacacacacaagacacaaaccaaaagacaac
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ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1076, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Ass
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1076
LENGTH: 7758
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US-10-311-455-1076/c
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Sequence 10, Application US/09827688

Publication No. US20030165476A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KINSEY, BERNA
APPLICANT: KINSEY, BERNA
APPLICANT: BHOGAL, BALBIR
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: AGENTS
FILE REFERENCE: P01949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR APPLICATION NUMBER: 60/195,680
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO: 100-10
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ORGANISM: RSV
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US-09-827-688-10
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT PEDLICATION UNGBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                      191 ATAGCCTCGGCAAACCACAAAGTCACATAACAACTGCAATCATACAAGATGCAACAAGC 250
                                                                                                                                                                                                                                             251 CAGATCAAGAACACAACCCCA-ACATACCTCACTCAGGATCCTCAGCTTGGAATCAGCTT 309
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                                                                                                   Length 793;
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9.3%; Score 85.8; DB 10; Length
Best Local Similarity 48.4%; Pred. No. 4e-12;
Matches 283; Conservative 0; Mismatches 300; Indels
; LOCATION: (1)...(793)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-C11
US-09-878-574-4304
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Publication No. US20030186277A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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; LOCATION: (379615)
US-10-312-841-2
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LENGTH: 3673778
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APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and other Molecules Associated with
TITLE OF INVENTION: Nucleic Acid Molecules and other Molecules Associated with
TITLE OF INVENTION: 191401) B
CURRENT APPLICATION NUMBER: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR PILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 4304
LENGTH: 793
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                                                                                Gaps
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                                                                            3;
                                        Length 7758;
                                      9.4%; Score 86.2; DB 12; Length 47.8%; Pred. No. 9.9e-12; ative 0; Mismatches 338; Indels
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                                                                          Matches 312; Conservative
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US-09-878-574-4304/c
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NAME/KEY: unsure
   US-10-311-455-1076
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Pred. No. 1.6e-11;
0; Mismatches 418;
                                                                                                                                                                                                                                                                                                   LOCATION: (1319)..[1328)
OTHER INFORMATION: a, t, c, g, unknown or other
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Best Local Similarity 45.4%;
Matches 350; Conservative
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                                                                         FRATURE:
NAME/KEY: CDS
LOCATION: (201) .. (1772)
FRATURE:
NAME/KEY: modified base
LOCATION: (975) .. (994)
OTHER INFORMATION: a, t, c
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NAME/KEY: modified_base
                                                          (1) \dots (1972)
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       FEATURE:
NAME/KEY:
LOCATION:
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al Similarity 47.0%; Pred. No. 2.8e-10; 334; Conservative 0; Mismatches 372; Indels
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ITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1981
LENGTH: 1972
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Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
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ORGANISM: Homo sapiens
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US-10-017-161-1981
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LOCATION: (4003, 5529, 5534, 5553, 5570, 5573, 5577..5578, 5592, 5732)
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46.6%; Pred. No. 2.5e-10;
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007
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                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 5012.1007
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03970
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
US-10-240-485-82/c
; Sequence 82. Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                          Sequence 1056, Application US/10311455
; Sequence 1056, Application US/2030143606A1
; Sequence 1056, Application No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by PLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR PLILING DATE: 2000-06-30
; PRIOR PLILING DATE: 2000-06-30
; PRIOR PLILING DATE: 2000-06-30
; PRIOR SEQ ID NOS: 2424
; SEQ ID NO 1056
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OTHER INFORMATION: n is a or g or c or t
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8.8%; Score 81.4; DB 12; Length 16167;
Best Local Similarity 46.6%; Pred. No. 2.5e-10;
Matches 235; Conservative 0; Mismatches 269; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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NAME/KEY: unsure
LOCATION: 5837..5838
OTHER INFORMATION: n is a or g or c or t
US-10-311-455-1056
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NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 16167
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### APPLICANT: OLEK, Alexander
### APPLICANT: DIEKOKCK, Christian
### APPLICANT: BISPENBROCK, Christian
### APPLICANT: BISPENBROCK, Christian
### APPLICANT: BISPENBROCK, Christian
### APPLICANT: BISPENBROCK, Christian
### TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
### TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
### TITLE OF INVENTION: With DNA TRANSCTIPTION
### TITLE OF INVENTION: With DNA TRANSCTIPTION
### PILLE OF INVENTION: WITH DATE: 2000-04-06
### PRIOR FILLING DATE: 2000-04-06
### PRIOR PILLING DATE: 2000-04-07
### PRIOR PILLING DATE: 2000-04-07
### PRIOR PILLING DATE: 2000-06-30
### PRIOR PILLING DATE: 2000-06-30
### PRIOR PILLING DATE: 2000-06-01
### PRIOR PILLING DATE: 2000-09-01
### PRIOR PILLI
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; Sequence 20, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 345; Conserv
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                                                  1996 ACTCCCTAÁACCCCTCAAAACAACCCTAACCTACACTCAAAAAATACTCTAAAAAT 1937
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734 ATCACAACTACACTGCTCACCAACAACGCACAGGAAATCCAAAAGCTCACAAGTCAAATG 793
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As:
TITLE OF INVENTION: cytosine methylation
FILE REPREBENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 378
                                                                                                                                              794 GAAACCITCCACTCAACCTCCTCC 817
                                                                                                                                                                                                                                                                                                ; Sequence 378, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                       -10-311-455-378/c
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Sequence 1670, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BEFEIN, Kurt
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT PRILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
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                                                                38 AAGACACTAGAAAAGACCTGGGACACTCTCAATCATTTATTATTCATATCATCGGGCTTA
                                                                                                                    2056 AACATACTCTAAAACACCCACGCAAACTCGCGTATAAAACTTATTCCTAAAACCTATCACT
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      0; Mismatches 415; Indels
      Matches 345; Conservative
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US-10-311-455-1670/c
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Publication No. US20030082609A1
| Publication No. US20030082609A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: DIER LANGE ABROCK, Christian
| APPLICANT: BERLIN, Kurt
| APPLICANT: BERLIN, Kurt
| TITLE REFERENCE: 5013.1003
| CURRENT APPLICATION NUMBER: US/10/239,676
| PRIOR APPLICATION NUMBER: US/10/239,676
| PRIOR APPLICATION NUMBER: PCT/EP01/03968
| DE 10019058.8 |
| DE 10019173.8 |
| DE 10019173.8 |
| DE 10019058.29.7 |
| DE 10004-06 |
| 2000-04-06 |
| 2000-04-06 |
| 2000-06-30
1756 AAAAAATTACTCAAAATAAAATATTACCCTCTACGAAAATTTAAAATCCCCTAACCTCC 1697
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                                                                                   CTCACTCAGGATCCTCAGCTTGGAATCAGCTTCTCC----AATCTGTCTGAAATTACAT 332
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Pred. No.
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ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 228
SEQ ID NO 12
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Best Local Similarity
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US-10-239-676-12/c
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OTHER INFORMATION: MAP TO ACO06647.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9
OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
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Pred. No. 5.3e-10;
0; Mismatches 398; Indels
                                                 PRIOR APLING DATE: 2000-09-27
PRIOR APLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2001-01-29
                                        IG DATE: 2000-09-27
CATION NUMBER: PCT/US01/00666
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ORGANISM: Homo sapiens
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 6668;
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Best Local Similarity 48.9%; Pred. No. 3.7e-10;
Matches 215; Conservative 0; Mismatches 225; Indels
                                                                                                                                                                                                                                                   ; NAME/KEY: unsure
; LCCATION: 1936
; CTHER INFORMATION: n is a or g or c or
US-10-311-455-1670
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Patent No. US200200048763A1
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                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1670
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8.5%; Score 78.2; DB 9; Length 1973;
Best Local Similarity 46.6%; Pred. No. 5.9e-10;
Matches 354; Conservative 0; Mismatches 398; Indels 7
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PRATURE: DNA
ORGANISM: Homo sapiens
PRATURE: INFORMATION: MAP TO ACO06547.9
OTHER INFORMATION: EXPRESSED IN LUNG. SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN HEAR, SIGNAL = 8.6
OTHER INFORMATION: EXPRESSED IN HEAR, SIGNAL = 9
OTHER INFORMATION: EXPRESSED IN HEAR, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN HEAR, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN POTAL LIVER, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2000-09-21

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

SEQ ID NO 3471

LENGTH: 1973
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US-09-864-761-3471
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APPLICANT: Rank, David R.
APPLICANT: Hank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        788 CARATGGAAACCTTCCACTCCACCTCCTCGAAGGCAATCTAAGC-CCTTCTCAAGTCTC 846
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TURENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELLING DATE: 2001-06-23
PRIOR PELLING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PPLICATION NUMBER: PCT/US01/00662
ILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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Patent No. US20020048763A1
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| ACCATCACTACCACCACCACC | CACAACATCCGAGCACCCATC | ACTÁCCACCACCACCACCATC |
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Search completed: October 30, 2003, 03:23:48 Job time : 319.043 sec8

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RESULT 1
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October 29, 2003, 21:37:29; Search time 71.4618 Seconds (without alignments) 5682.373 Million cell updates/sec
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/cgm2_6/ptodata/2/ina/PCTUSCOMB.seq:*
/cgm2_6/ptodata/2/ina/PCTUSCOMB.seq:*
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-872-969A-7

US-08-467-969A-7

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US-08-001-554A-7

US-08-901-554A-7

US-08-901-58A-7

US-08-801-898A-23

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq
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APPLICANT: KLEIN, Michel H
APPLICANT: KLEIN, Michel H
APPLICANT: TO, Kun.-Pan
APPLICANT: DI, Kun.-Pan
APPLICANT: DI, Kun.-Pan
APPLICANT: DI, Kun.-Pan
APPLICANT: DI, Kun.-Pan
APPLICANT: BRASYSHYN, MATY E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: ARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
ADDRESSE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                              Appli
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Sequence 3, A
Sequence 14,
Sequence 14,
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
US-08-836-504A-3
US-08-836-501-3
US-09-654-896-3
US-09-628-876-3
US-08-08-10-979A-14
US-08-10-14
US-09-654-289-14
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US-09-654-289-14
US-09-654-289-14
US-09-651-14
US-09-651-14
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US-08-836-501-23
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US-09-654-289-23
US-09-654-28
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APR-1997
FILING DATE: 06-JAN-1993
FRIOR APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1992
ATTORNEY/AGNET INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/COCKET NUMBER: 24,973
REFERENCE/COCKET NUMBER: 1038-474 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPAK: (416) 595-1155
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Patent No. 5968776
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i LENGTH: 920 base pairs
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Sequence

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Patent No. 5998169

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Length 920;
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100.0%; Score 920; DB 2; I 100.0%; Pred. No. 8.8e-243;
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US-08-838-189D-7
; Sequence 7, Application US/08838189D
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Best Local Similarity 100.
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GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: TOU, Run-Pan
APPLICANT: BRASYSHYN, MARY E
TITLE OF INVENTION: WULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CACTCTCAATCATTTATTCATATCATCGGGCTTATATAAAGTTAAATCTTAAATCTGT
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                                                                                                                                                       CONDESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 920; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 8.8e-243;
Matches 920; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                FILING DAILS

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
FELECOMMUNICATION INFORMATION:
TELEFORM (416) 595-1165
TELEFORM (416) 595-1165
TELEFAX: (416) 595-1165
TELEFAX: (416) 595-1167
SEQUENCE CHARATERICHICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-838-189D-7
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                               FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REERRENCE/DOCKET NUMBER: 1038-688 MIS:jb
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
                            GB 9200117.1
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TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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                                                                    AACACCAGGAGTCAAGTCAAACCTGCAAACCCACAAAGTCAAGAACTAAAAAACACAACAAC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: DU, RULPEN
APPLICANT: DU, RULPEN
TITLE OF INVENTION: CHIMBERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF EXQUENCES: 3
CORRESPONDENCES: 31
ADDRESSEE: SIM & McBuiney
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STATE: Obtain

COUNTRY: Canda

ZIP: MSG 1RF.
COMPUTER READABLE FORM:

MEDTUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

CORPATER: PER PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,344D

FILING DATE: 07-MAY-1997

CLASSIFICATION 1424

PRIOR APPLICATION NUMBER: US 08/344,639

FILING DATE: 14-NOV-1994
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6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAGTTATTAAAAAAAAA 920
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Patent No. 6017539
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US-08-852-344D-7
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              CACAAGTCAAATGGAAACCTTCCACTCCTCCCGAAGGCAATCTAAGCCCTTCTCA
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                                                                                                                                                                                                                                Sequence 7, Application US/0834639E

Patent No. 6033668
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reasyn, Mary B
APPLICANT: Bwasyshyn, Mary B
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF SEQUENCES: 38
CORRESPONDENCE: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 920; DB 3; Length 920; 100.0%; Pred. No. 8.8e-243; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Canada

ZIP: MSG 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 06-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
RIUNG DATE: 06-JAN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: Stewart, Michael I
REGISTRATION NUMBER: 1038-391 MIS
TEMECOMMINICATION NUMBER: 1038-391 MIS
TEMECOMMINICATION NUMBER: 1038-391 MIS
TEMECOMMINICATION NUMBER: 1038-391 MIS
                                                                                                                                                                                                                                                                                                                                                                                                                     330 University Avenue, 6th Floor
                                                                                                                                   GTAGTTATTAAAAAAAA 920
                                                                                                                                                                Gragirarrahahahahaha 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1153
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 920; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 330 Uni
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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61 CACTCTCAATCATTTATTATTCATATCATCGGCCTTATATAAGTTAAATCTTAAATCTGT 120
                                                                                12.1 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08467969A
Patent No. 6168786
GENERAL INPORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
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999 720 720 780 780 840

480 540 540 900 600

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900

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661 AACCACTAAACCAAAGGAAGTACCCACCAAGCCCACAGAAGAGAGCCAACCATCAACAC 720
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                                                                                                                                                                                                                                       601 CACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAAGATCTCAAACCTCA
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                                                                                                                                                                                                                                                                           ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6TH Floor
STATE: Ontario
COUNTRY: Canada
ZATE: Ontario
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
PRICK APPLICATION: 435
PRICK APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08467961A
Fatent No. 6171783
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION: 4335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILLING DATE: 06-JAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart Mich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 GTAGTTATTAAAAAAAAA 920
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                                                                                                   STATE: OLICATION
COUNTRY: Canada
ZID: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
FILING DATE: 06-JAN-1992
CLASSIFICATION: MATA:
APPLICATION: MATA:
APPLICATION: A35
FILING DATE: 06-JAN-1992
CLASSIFICATION: A35
FILING DATE: 06-JAN-1992
                           ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038-475 MIS:bh
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NAME: Stewart, Michael I
REGIESTRATION UNDHER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELEPOWNINICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 920; Conservative
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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330 University Avenue, 6th Floor
                                                                                       GTAGTTATAAAAAAAA 920
                                                                                                                                                                                             ; Sequence 7, Application US/08001554A; Patent No. 6225091
                                                                                                                    901 GTAGTTATTAAAAAAAAA 920
                                                                                                                                                                                                                                            APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Climeric In
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                            Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 920, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                      STREET: 330 Unive
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-001-554A-7
                                                                                                                                                                   RESULT 7
US-08-001-554A-7
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                                                                                                                                                                                                                               100.0%; Score 920; DB 3; Length 920; 100.0%; Pred. No. 8.8e-243; Live 0; Mismatches 0; Indels
         REFERENCE/DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
TELER: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
ILENGTH: 920 base pairs
TYPE: nucleic acid
STRANDENNES: single
REGISTRATION NUMBER: 24,973
                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 920; Conservative
                                                                                                                                                                                                    US-08-467-961A-7
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781 CACAAGTCAAATGGAAACCTTCCACTCCACTCCTCCTGAAGGCAATCTAAGCCCTTCTCA 840 900 120 120 180 CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA 240 09 9 841 AGTCTCCACAACATCCGAGCACCCATCACAACCCTCATCTCCACCCAACAACAACACACGCCA 1 TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGA 121 AGCACAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGC 121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGC CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA 1 TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGA 61 CACTCTCAATCATTATTATTCATCATCGGGCTTATATAAGTTAAAATCTTAAATCTGT Gaps . 0 Length 920 100.0%; Score 920; DB 3; Length 9 100.0%; Pred. No. 8.8e-243; Ative 0; Mismatches 0; Indels COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWARL/AGENT INFORMATION:
REGISTRATION NUMBER: 24,973
REFRERENCE/DOCKET NUMBER: 1038-286
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 595-1153
TELERAX: (416) 595-1163
TELERAX: (416) 595-1163
TELERAX: G165-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 basits

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61 AATCATITATITATICATATCATCGGGCTIAIATATATAAGTIAAATCTIAAATCTGTAGCACAA 120
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 894; DB 2; Lr
Pred. No. 1.2e-235;
                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/638,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART MCARALION:
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-474 MIS:jb
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
SEQUENCE CHARACTELS:
SEQUENCE CHARACTELS:
TELEPHONE: (416) 595-1163
TELEPHONE: CHARACTELS:
TELEPHONE: 004 No. 28:
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97.2%; Score 894; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 894; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-467-963C-28
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APPLICANT: KLEIN, Michel H
APPLICANT: DU, Kun-Pan
APPLICANT: DU, Kun-Pan
APPLICANT: DI, Kun-Pan
APPLICANT: CHIMBRIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAGGAA
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                                                                                                                                                                    AACACCAGGAGTCAAGTCAAACCTGCAACCCACAAGACCAAAGACTAAAAACACAACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08467963C Patent No. 5968776
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ADDRESSEE: Sim & MCB
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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US-08-467-963C-28
                                                  241
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                                    TTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACA
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APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
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; Sequence 28, Application US/08852344D
; Patent No. 6017539
; GENERAL INFORMATION:
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APPLICANT: KLEIN, Michel H
APPLICANT: EWASYSTRYN, Mary E
APPLICANT: BWASYSTRYN, MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMBRIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMBRIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: TOTORIO
STRATE: Ontario
CITY: Canada
                                                                                                                                                                                                              781 CAAATGGAAACCTTCCACTCCACTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCC
661 AAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAAGCCAACCATCAACACCACAAA
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                                                    AAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAGCCAACCATCAACACCACCAAA
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:

NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-687 MIS:jb
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 28:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08838189D Patent No. 5998169
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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MSG 1R7
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US-08-838-189D-28
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788 CAAATGGAAACCTTCCACTCAAACCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTC
          188 AATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCA
                                                                                                            668 AAACCAAAGGAAGTACCCACCACCAAGCCCACAAGAAGAGCCAACCATCAACACCACCAAA
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APPLICANT: Klein, Michel H
APPLICANT: Klein, Michel H
APPLICANT: Basyshyn, Mary E
APPLICANT: Basyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA
TITLE OF INVENTION: DAD AND RESPIRATORY SYNCTTIAL VIRUS
NUMBER OF SEQUENCES: 38
COMPRESSONDENCES: 38
COMPRESSONDENCES: 38
COUNTRY: Canada
ZITY: TOTONICO
STRATE: Ontario
STRATE: Ontario
COUNTRY: Canada
ZITY: MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Prophy disk
COMPUTER: DAD FORDICAL SOS /MS-DOS
SOSTWARE: DATE 14-NOV-1994
CLASSIFICATION NUMBER: US 08/001,554
FILING DATE: 14-NOV-1993
CLASSIFICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: B 29200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: 24,973
REFERENCE/OCKET NUMBER: 13,973
REFERENCE/OCKET NUMBER: 13,973
REFERENCE/OCKET NUMBER: 13,973
REFERENCE/OCKET NUMBER: 13,973
TELECOMMUNICATION HUMBER: 14,165
TELECOMMUNICATION HUMBER: 16,165
TELECOMMUNICATIO
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Patent No. 6033668
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US-08-344-639E-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 TICATAGCCICGCCAAACCACAAAGICACACTAACAACTGCAATCATACAAGATGCAACA 247
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                                                                                                       STATE: Uncarlo
COMPUTRY: Canada
ZIP: MGG 1R7
COMPUTRY: READABLE FORM:
MEDIUM TYPE: PLODBY disk
COMPUTER PLODBY disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/344,639
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 06-JMN-1994
FRIOR APPLICATION NUMBER: US 08/344,639
FILING DATE: 10-1994
FRIDKS APPLICATION NUMBER: US 08/344,639
FRIDKS APPLICATION NUMBER: US 08/344,639
FRIDKS APPLICATION NUMBER: US 05-JN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 1038-688 MIS:jb
TELECOMMUNICATION NUMBER: 11038
TELEFRAX: (416) 595-1163
INFORMATION FOR SEG ID NO: 28:
FENCTH: 894 base pairs
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 894; Conservative
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                        ADDRESSEE: Sim
STREET: 6th Flo
CITY: Toronto
                                                                                                 STATE: Ontario
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US-08-801-898A-23
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                                                                                                                        97.2%; Score 894; DB 3; Length 894; 100.0%; Pred. No. 1.2e-235;
                                                                                                                                   100.0%; Pred. ...
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                       Best Local Similarity 100.
Matches 894; Conservative
                                                                               linear
                                                                                           US-08-344-639E-28
                                                                             TOPOLOGY:
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US-08-801-898A-23

Sequence 23, Application US/08801898A

Patent No. 598602

GENERAL INFORMATION:
PAPLICANT: Torrence, Paul F.
APPLICANT: Silverman, Robert H.
APPLICANT: Cirino, Nick M.
APPLICANT: Li, Guiying
APPLICANT: Li, Guiyi
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,898A
FILING DATE: 18-FEB-1997
CLASSIFICATION: 514
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NAME: Poissant, Brian M.
REGISTATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8656-009
TELECOMMUNICATION INFORMATION:
TELERPHONE: 212-790-9090
TELERAX: 212-869-9741
TELEX: 66.41 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 15.22 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: SINGle
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Matches 878; Conservative
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LOCATION: 1..15222
OTHER INFORMATION:
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RESULT 14
US-08-892-403A-1
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Batent No. 6214805

GENERAL INFORMATION:

APPLICANT: SIlverman, Robert H.

APPLICANT: Cirino, Nick M.

APPLICANT: Li, Guiying

APPLICANT: Li, Guiying

APPLICANT: Li, Guiying

APPLICANT: Player, Mark R.

ITILE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLICONUCLEOTIDES

ITILE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE

CURRENT APPLICANT: 1997-11-03

FILE REFERENCE: 8656-019

CURRENT FILING DATE: 1997-11-03

EARLIER APPLICATION NUMBER: 08/801, 896

EARLIER APPLICATION NUMBER: 60/011,725

EARLIER PILING DATE: 1996-02-15

NUMBER OF SEQ ID NOS: 40

SEQ ID NO 12

MANDER OF SEQ ID NOS: 40

SEQ ID NO 12

MANDER OF SEQ ID NO 12
aacaccaggagtcaagtcaaacctgcaacccacacagtcaagactaaaaacacaacaac
                               ACCCAATAATGATTTTCACTTTGAAGTGTTCAACTTTGTACCCTGCAGCATATGCAGCAA
                                                                                                                      ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTTGTACCCTGCAGCATATGCAGCAA
                                                                                                                                 CACCAAAACAACATCACAACTACACTGCTCACCAACAACACCCACAGGAAATCCAAAACT
                                                      ; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-08-962-690-12
                                                                                                                                                                                                                                                                                                                                     CTAGTTACTTAAAAACATA 5599
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US-08-962-690-12/c
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                                Gaps
   Length 15222;
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                              Indels
                              41;
 Score 853.4; DB 3;
Pred. No. 5.4e-224;
0; Mismatches 41;
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Query Match
Best Local Similarity 95.5%;
Matches 878; Conservative
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FATENT NO. 9.25.95.97

FATENT NO. 9.25.95.97

FITLE OF INVENTION: PRODUCTION OF INFECTIOUS RESPIRATORY

TITLE OF INVENTION: PRODUCTION OF INFECTIOUS RESPIRATORY

TITLE OF INVENTION: SINCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS: 1

CORRESPONDENCES: 1

CONFORMENT: Two Embarcadero Center, 8th Floor

STATE: CA

COUNTRY: U.S.A.

CONFORMER: Tan Paradisco

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 27-SEP-1996

CLASSIFICATION: 424

FRIOR APPLICATION DATA:
                                                                                                                    420
4922 TGCAACAAGCCAGATCAAGAACACACCCCAACATACCTCACCCAGAATCCTCAGCTTGG 4981
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US-08-720-132-1
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                                 APPLICANT: Murphy, Brian R.
APPLICANT: Collins, Peter L.
APPLICANT: Collins, Peter L.
APPLICANT: Mittehead, Stephen S.
APPLICANT: Dukreyev, Alexander A.
APPLICANT: Dukreyev, Ratalin
TITLE OF INVENTION: SYNCYTIAL VIRUS VACCINES FROM CLONED NUCLEOTIDE SEQUENCES NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1682 IGCARACATGTCCARARCAAGGACCAACGCACGCTAAGACATTAGAAAGGACCTGGGA 4741
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MEDIUM TYPE: 10.984

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,403A
FILING DATE: 15-MUL-1997
CLASSIFICATION NUMBER: US 60/047,634
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,141
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,141
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 60/021,773
FILING DATE: 15-UL-1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 17634
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15223 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 95.5
Matches 878; Conservative
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GENERAL INFORMATION:
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Search completed: October 30, 2003, 01:17:36
Job time : 74.4618 secs
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                                                                                                                                                                                                     Score 853.4; DB 3;
Pred. No. 5.4e-224;
0; Mismatches 41;
*** FEFLING DATE: 27-SEP-1995
*** ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
*** REFERENCE/DOCKET NUMBER: 15280-250-1
TELEDENONE: 206-467-9600
TELEPRAY: 415-576-0300
*** TELEPAX: 415-576-0300
*** INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
*** ELENGTH: 15223 base pairs
TELENTH: 15223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOJ.KCTHE
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Best Local Similarity 95.5%;
Matches 878; Conservative 0
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US-08-720-132-1
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                                                                                                                                A novel multimeric hybrid gene is used as a vaccine. The gene consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus (RSV)). The gene sequences that are particularly used are those which encode PIV-3 F and HN proteins (AAQ45684) and RSV F and (Updated on 25-MAR-2003 to correct PN field.)
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para-influenza virus and respiratory syncytial virus
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                                                                         Multimeric hybrid genes and their chimeric proteins
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Matches 920; Conservative 0
         (CONN-) CONNAUGHT LAB LTD
                            Klein MH
                                              WPI; 1993-243222/30.
P-PSDB; AAR39286.
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 administered to a host organism. The composition is useful as a vacchine to immunise against RSV-associated disease, particularly resulting in a balanced Thl/Th2 immune response and for raising by usual immunisation and cell fusion methods.
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                                                                   100.0%; Score 920; DB 20; Length 920; 100.0%; Pred. No. 1.4e-211; ive 0; Mismatches 0; Indels 0.
                                                 Sequence 920 BP; 380 A; 290 C; 95 G; 155 T; 0 other;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV vaccines. The vaccine can be administered to pregnant women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccines for human respiratory virus - comprising proteins or fragment encoded by a DNA sequence coding for human respiratory syncytial virus proteins.
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                                                                                                                                                  Sequence encoding human respiratory syncytial virus (HRSV) A2
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Pred. No. 1.4e-196;
0; Mismatches 39;
                                                                                                                                                                                                                 Human respiratory syncytial virus (HRSV)
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                                                                BP.
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                                                              AAN70784 standard; cDNA; 935
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Best Local Similarity 95.8%;
Matches 881; Conservative
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P-PSDB; AAP70845.
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                                                                                                                                                                                                                                               Production of human respiratory syncytial virus glyco-protein F or G
- by culturing eukaryotic host cells transfected with corresponding
DNA.
                                                                                                                                                                                                                                                                                                                                                                      The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare
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Pred. No. 1.4e-196;
0; Mismatches 39; Indels
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                      86US-0818740.
86WO-US02756.
92US-0897171.
97US-0854783.
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Best Local Similarity 95.8%;
Matches 881; Conservative
                                                                                                                    (PHAA ) PHARMACIA & UPJOHN
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P-PSDB; AAW47605.
                      14-JAN-1986;
23-DEC-1986;
11-JUN-1992;
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                                       The sequences of mRNA encoding HRSV structural proteins are given in AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                 ;
                                                                                                                                                 Query Match 93.0%; Score 856; DB 13; Length 935; Best Local Similarity 95.7%; Pred. No. 3.4e-196; Matches 880; Conservative 0; Mismatches 40; Indels
                                                                                                                            Sequence 935 BP; 382 A; 294 C; 100 G; 159 T; 0 other;
                   Disclosure; Page 18; 21pp; English.
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                                                                                                       CACCAAAACAAACATCATAACTACACTCACCTCCAACACACACAGGAAATCCAGAACT
                                                                                                                                                                                                       AGTOTOTACAACATCCGAGTACCCATCACAACCTTCATCTCCACCCAACACACGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines for human respiratory virus - include structural genes coding for native structural viral proteins and immunogenic fragments
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P-PSDB; AAR25302.
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13-JUL-1988;
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5521 AGTCTCTACAACATCCGAGTACCCATCACAACCTTCATCTCCACCCAACACACCACGCCA
 4801 AGCACAAAATCACATTCTCTGGCAATGATAATTTCTCAACTTCAACTTTATAATTGCAGC
                                                                                                                         4921 IGCAACAAGCCAGAICAAGAACACAACCCCAACAIACCTCACCCAGAAICCTCAGCTIGG
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                                                            AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAGCTTCAAC
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                                              CATCATATTCATAGCCTCGGCAAACCACAAAGTCACACTAACAACTGCAATCATACAAGA
                                                                                                        TGCAACAAGCCAGATCAAGAACACACCCCCAACATACCTCACGATCCTCAGCTTGG
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849 AGTCTCTACAACATCCGAGGGACCTACAACCTTCATCTCCACCCAACACACGCCA 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in the preparation of a novel polynuclectide, comprising an antisense oligonuclectide, with a hydroxy group at one end, that is complementary to 15-20 bases of the anti-genomic RNA strand of a respiratory syncytial virus (RSV), a linker attached to the OH-end of the antisense oligonuclectide and an oligonuclectide activator of RNaseL attached to the linker. The polynuclectide can be used to treat RSV infections, which can also be treated by administration of the antisense oligonuclectide, so as to form a complex with activated RNase L in vivo. The polynuclectide can be transported across the cell membranes without carriers or permeability agents, and once introduced destroys antisense target RNA. It also inhibits RSV infection in vitro in a superior manner to the conventional drug, ribavirin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide containing sequence anti-sense to region of RSV -
connected via a linker to an activator of RNaseL, used to treat RSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.8%; Score 853.4; DB 18; Length 15222; 95.5%; Pred. No. 3.2e-195; Live 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15222 BP; 5923 A; 2706 C; 2356 G; 4237 T; 0 other;
                                                                                                                                                                                                                                                                        respiratory syncytial virus; inhibition; strain A2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Torrence PF,
                                                                                                                                                                                                                                           Human respiratory syncytial virus strain A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Pages 47-51; 89pp; English
                                                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus
                                              901 GTAGTTATTAAAAAAAA 920
                                                                         909 Gradriacrirahahahaha 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cirino NM, Li G, Silverman RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLEV-) CLEVELAND CLINIC FOUND (USSH ) US NAT INST OF HEALTH.
                                                                                                                                                   AAT78440 standard; DNA; 15222
                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0011725.
                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US02531
                                                                                                                                                                                                                                                                       Antisense oligonucleotide;
RSV; treatment; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 95.5
Matches 878; Conservative
                                                                                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-424748/39
                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infections
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                                                                                                                                                                               AAT78440;
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                                                                                                                      RESULT 6
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5522 AGTCTCTACAACATCCGAGTACCCATCACAACCTTCATCTCCACCAACAACACCACGCGCA 5581
                                                                                                                             5282 CACTACCAAGCCCACAAAAAAACCAACCTCAAGACAACCAAAAAAAGATCCCAAAAACCTA
                                                                                                          AACCACTAAAACCAAAGGAAGTACCCACCACCACGAGGAGGAGGAGGAGCAACCATCAACAC
                                                                                                                                                                               CACCAAAACAAACATCACAACTACACTGCTCACCAACAACACCACAGGAAATCCAAAAACT
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                                                                                                                                                                                                                                                                                             CACAAGTCAAATGGAAACCTTCCACTCCACTCCTCCGAAGGCAATCCAAGCCCTTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - useful to protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respiratory syncytial virus (RSV) D46. The genome is negative-sense; the complete nucleotide sequence of the wild-type B-1 virus has also been determined (see AAV17552). A novel infectious recombinant RSV comprises a RSV genome or antigenome, a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a large polymerase protein (L), and a RNA polymerase elongation factor, where the recombinant RSV has at least two attenuating mutations, one of the mutations specifying temperature-sensitive (ts) substitution at amino acid Phe521,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the 5'-3' positive sequence nucleotide sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSV; attenuation; vaccine; pneumonia; bronchiolitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Attenuated respiratory syncytial virus vaccines individuals against RSV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 188-195; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syncytial virus antigenome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus D46.
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96US-0021773.
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Whitehead SS;
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09-MAY-1997;
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                                                                                                                                                                                                                                                                                                            genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                            Infectious respiratory syncytial virus particles - useful for treatment of RSV or gene therapy of upper respiratory tract diseases
                                                                                                                                                                                                                                                                              A human respiratory syncytial virus (RSV) anti-genome sequence (AAT63430) is the 5' to 3' positive-sense sequence of RSV; the genom itself is negative-sense. It was synthesised in segments by RT-PCR using intracellular RSV mRNA or genomic rRNA isolated from purified viruses as template. Restriction site markers were intoduced by incorporating the changes into the primers used for RT-PCR. The recombinant sequence can be expressed with a nucleocapsid protein, a large polymerase protein and an an uncleocapsid phosphoprotein, a large polymerase protein and an RNA elongation factor to produce isolated infectious RSV particles useful for generating vaccines against RSV. Recombinant RSV genome or antigenome can also be used as a vector for gene therapy of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 15223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.8%; Score 853.4; DB 18 95.5%; Pred. No. 3.2e-195;
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                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                 Claim 46; Page 43-51; 66pp; English,
             96WO-US15524
                                               95US-0007083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          upper respiratory tract.
                                                                                                                                                        WPI; 1997-212893/19.
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Matches 878; Conser
             27-SEP-1996;
                                               27-SEP-1995;
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Gin831, Metil69 or Tyri321 in the RSV polymerase gene or a ts nucleotide substitution in the gene-start sequence of gene M2.
Also claimed are: (1) an isolated infectious RSV particle which comprises a recombinant RSV (anti) genome, N, P, and L proteins, a RNA polymerase elongation factor, where the (anti)genome is modified: (i) to ablate or modulate expression of a SH, NSI, NS2 or G gene or a cis-acting regulatory sequence; and (11) by a termination codon introduced within a selected gene, or by a change in sequence, position or presence of a GS or GB transcription signal relative to the selected gene; (2) an expression vector; and (3) an RSV strain selected from cpts RSV 248 (Arcc WR 2450), cpts 248/404 (Arcc VR 2451) cpts RSV 530 (Arcc VR 2452), cpts RSV 530/1009 (Arcc VR 2451) or cpts 530/1009 (Arcc VR 2451) or cpts 530/1009 (Arcc VR 2451) or cpts 530/1009 (Arcc VR 2452) or B-1 cp52/2B5 (Arcc VR 2451) or cpts 530/1030 (Arcc VR 2452), or B-1 cp52/2B5 (Arcc VR 2451) or cpts 530/1030 (Arcc VR). The isolated attenuated recombinant RSV and RSV particles are used in a vaccine to stimulate the immune system of an individual to induce to stimulate the immune system of an individual to induce to stimulate the immune system of an individual to induce to stimulate the immune system of an individual to induce to protection against RSV. The expression vector of (2) is used for the production of infectious attenuated RSV particles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CACTCTCAATCATTAATTATTCATATCATCGGGCTTATATAAAGTTAAAATCTTAAATCTGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                     92.8%; Score 853.4; DB 19; Length 15223; 95.5%; Pred. No. 3.2e-195; ive 0; Mismatches 41; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                  Sequence 15223 BP; 5921 A; 2704 C; 2361 G; 4236 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.57
Watches 878; Conservative
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    in the NS2-N intergenic region"
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replace (1140, G)
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replace (5612, A)
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1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of human respiratory syncytial virus (RSV); the genome itself is negative-sense. This antigenome cDNA, termed D46, was structested in segments by RT-PCR using synthetic oligonucleotides as primers and intracellular RSV mRNA or genome RNA isolated from purified virions as template. The antigenome includes a S'-terminal noriviral Gtriplet contributed by the T7 promoter, 4 sequence markers (see AAA88745-47) at positions 1099 (which adds 1 nucleotide to the length), 1139, 5611 and 7559, a ribozyme and tandem T7 terminators, and a single norviral 3'-phosphorylated residue contributed to the 3' end by ribozyme cleavage. The invention provides an isolated infectious chimeric RSV comprising a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a nucleocapsid (N) protein (L), an RNA polymerase elongation factor, and a partial or complete RSV genome or antigenome of one RSV strain or subgroup virus. The chimeric RSV is a chiferent RSV strain or subgroup virus combined with a heterologous gene of a chiferent RSV strain or subgroup virus. The chimeric RSV is a nutations. It is useful as a vaccine against RSV, which causes diseases such as pneumonia and bronchiolitis in infantes. The chimers system of an individual is stimulated to induce protection against natural RSV infection, preferably in a multivalent manner to achieve protection against multiple RSV strains and/or subgroups.
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cloned nucleotide sequences, useful as a vaccine against diseases caused by the virus, such as pneumonia and bronchiolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cch 32.8%; Score 853.4; DB 21; Length 15223; al Similarity 95.5%; Pred. No. 3.2e-195; 878; Conservative 0; Mismatches 41; Indels 0; (
                                                                                                     present sequence is that of the 5' to 3' positive-sense
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                                                           Example 7; Page 262-268; 280pp; English
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Best Local Similarity
Matches 878; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against respiratory syncytial virus (RSV), comprises a sequence adapted for expression in plants and a RSV protein or peptide coding sequence
                                                                                           CACCAAAACAAACATCACAACTACACTGCTCACCAAAACAACACCACAGGAAATCCAAAACT
                                                                                                                                                                                 CACAAGTCAAATGGAAACCTTCCACTCCACCTCCGAAGGCAATCTAAGCCCTTCTCA
                                                                                                                                                                                                                                     661 AACCACTAAACCAAAGGAAGTACCCACCACCACACACAGAGAGCCAACCATCAACAC
                                                                                                                                                                                                           5462 cacaagrcaaargcaaaccrrccacrcaacrrccaaggcaarccaagcccrrcrca
                        601 CACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAAGATCTCAAACCTCA
                                                                                                                                                        The present invention relates to a chimeric nucleic acid construct comprising: a nucleotide sequence adapted for protein expression in plants; and a respiratory syncytial virus (RSV) coding sequence encoding an RSV protein or an antigenic protein or peptide of RSV. The construct can be used to immunize animals and humans against respiratory syncytial virus. The use of transgenic plants to generate the antigen allows the production of greater amounts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric nucleic acid construct for immunizing animals and humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric, respiratory syncytial virus, RSV; immunize, ds.
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                                                                                                                                                                                                                                                                                                                   5582 Gradriaciraaaacara 5600
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                                                 TGCAAACATGTCCAAAAACAAGGACCAACGCACGGCTAAGACTAGAAAAGACCTGGGA
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                         Gaps
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 Length 918;
92.2%; Score 848.2; DB 22; Length
95.8%; Pred. No. 2.6e-194;
ive 0; Mismatches 38; Indels
                         Matches 871; Conservative
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AAS20145 standard; DNA; 897 BP

RESULT 11 AAS20145 ID AAS2 XX

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The invention relates to a recombinant Sendai virus comprising an exogenous nucleic acid encoding a paramyxovirus (PWV) protein or its antiquenc fragment. The virus may be administered in combination with an antiviral chemotherapeutic compound. Two or more viruses expressing different PWV proteins nay be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PWV in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous nucleic acid encoding a second PWV protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PWV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral vector encoding a PWV protein. The recombinant virus is useful as an effective vaccine against hPIV or RSV (the major causes of paediatric respiratory disease) and also to express any gene of impact on impaired cells, Mild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or beta-
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                                                                                                              RSV, de; G protein; heavily glycosylated protein; antianaemic; antiviral; vaccine; gene therapy; paramyxovirus; sendai virus; PWV; antiviral chemotherapeutic compound; humoral response; cellular immune response; hPIV; paediatric respiratory disease; globin gene transfer; sickle cell disease; beta-thalassaemia; human immunodeficiency virus infection; HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Sendai virus useful in vaccines to protect infection paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment
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Pred. No. 8e-192;
0; Mismatches 37; Indels 0;
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                                                                               syncytial virus G protein DNA.
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                                                                                                                                                                                                                                                               Human respiratory syncytial virus
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Matches 860; Conservative
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The specification describes a composition comprising a polynucleotide consisting of an antisense oligonucleotide containing a hydroxy group, complementary to the genomic or antigenomic strand of a negative-strand RNA virus, and an activator of RNSse L. The polynucleotide is used to inhibit, or treat, infection by negative-strand RNA viruses, specifically respiratory syncytial virus (RSV) but also (para)influenza, mumps, and rables. The polynucleotide can cross cell membranes without requiring carriers or permeabilizing agents, and can selectively cleave the RNA targeted by the oligonucleotide. The present sequence represents New composition useful for inhibiting or treating infections against negative-strand RNA virus Sequence 15210 BP; 4232 A; 2351 C; 2700 G; 5919 T; 8 other; PF; Torrence G, Player MR, Silverman RH, Disclosure; Fig 1; 98pp; English. FOUND (USSH) US NAT INST OF HEALTH 97US-0962690. syncytial virus. (CLEV-) CLEVELAND CLINIC WPI; 1999-326917/27. Cirino NM, Li 02-NOV-1998; 03-NOV-1997; HO9922742-A1 Respiratory 14-MAY-1999 Xiao W;

Query Match

90.3%; Score 830.4; DB 20; Length 15210;
Best Local Similarity 94.6%; Pred. No. 1.1e-189;
Matches 869; Conservative 3; Mismatches 41; Indels 6; Gaps

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The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative
        Claim 8; Figure 3; 67pp; English
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                                                                    CACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAAACCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic composition for generating antibodies against respiratory syncytial vitus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                       G protein; respiratory syncytial virus; RSV; recombinant vector; vaccine; immune response; immunogenicity; tPA; antibody; tissue plasminogen activator; ss.
                                                                                                                                                                                                                                                                                                                                                                        G protein gene fragment of respiratory syncytial virus.
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produced may also comprise the signal peptide of tissue plasminogen activator (LPA). The recombinant vector may also comprise the signal peptide of tissue plasminogen activator (LPA). The recombinant vector may also comprise sequences immunoprotective ability. The resulting immunogenic composition will agenerate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly by usual immunisation and cell fusion methods.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                    77.7%; Score 715; DB 20; Length 715; 100.0%; Pred. No. 2.5e-162; Artive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                    Sequence 715 BP; 305 A; 240 C; 70 G; 100 T; 0 other;
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247 240

360

546 540 909

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AGCCAGATCAAGAACACAACCCCAACATACCTCAGGATCCTCAGGTTGGAATCAGC 307
                                                                                                                              TTCTCCAATCTGTCTGAAATTACATCACAACCACCACCATACTAGCTTCAACAACACCA 367
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                                                     TTCATAGCCTCGGCAAAACCACAAAGTCACACTAAAAACTGCAATCATACAAGATGCAACA
                                                                                                                                                                                       301 CCCTCTAATCCGTCTGAAATTACATCACAAATCACCACACATAGCTTCAACAACAACACA
                                                                                                                                                                                                                           GGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAACACAACAAC-AACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                         TAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Attenuated respiratory syncytial virus vaccines - useful to protect individuals against RSV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attenuation; vaccine; pneumonia; bronchiolitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Teng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAACCAAAGGAAGTACCCACCACCAAGCCC 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus B-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins PL, Juhasz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory syncytial virus genome.
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96US-0021773.
97US-0046141.
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09-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Such that when an in-frame fusion is made, the resultant fusion protein may be transported to, and anchored in, a mammalian cell membrane where it can be exposed to the host immune system.

Insertion of pneumococcal surface protein A (PspA) coding sequence created plasmid pKSD2601 intramuscular immunisation of BALB/c created plasmid pKSD2601 intramuscular immunisation of BALB/c created plasmid pKSD2601 induced protection against an otherwise lethal challenge with a capsular type 3 pneumococcus. A claimed plasmid for expression of pneumococcal epitope DNA in eukaryotic cells includes a promoter for driving expression in a eukaryotic cell ce.g. HCWV-LE, DNA encoding a leader sequence (e.g. of R&VG) and DNA encoding a leader sequence (e.g. of R&VG) and DNA encoding a pneumonoccal epitope such as PspA. The invention also provides a vaccine comprising the plasmid and a suitable carrier or diluent, and optionally one or more cytokines or DNA encoding them, or a bacterial delivery system. The vaccine is used to elicit an immunological response in a host, including humans, susceptible to pneumococcal infection or sepsis. The plasmid can also be used to express a pneumococcal epitope of interest in vitro.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTCCAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGACACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a portion of the respiratory syncytial virus glycoprotein G (RSVG) gene. It has been inserted into plasmid pcDNA3 (see AAV38297) to create plasmid pcT4. This plasmid contains a human cytomegalovirus immediate early promoter and the RSVG gene portion
                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid containing pneumococcal epitope for expression in eukaryotic cells - useful for eliciting immunological response to pneumococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                RSV; glycoprotein G; pneumococcal surface protein A; PspA;
infection; Streptococcus pneumoniae; sepsis; otitis media;
meningitis; bacteraemia; pneumonia; vaccine; genetic immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels
                                                                                                       Respiratory syncytial virus glycoprotein G gene portion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 696 BP; 284 A; 211 C; 78 G; 123 T; 0 other;
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al Similarity 96.1%;
664; Conservative
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Example 4; Page 195-202; 238pp; English.

XX
XX
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CC This is the complete mucleotide sequence of the wild-type B-1
respiratory syncytial virus (RSV). The genome is negative-sense;
the 5-3; positive-sense sequence of D46 is provided in AAVI7533.

CC Anovel infectious recombinant RSV comprises a RSV genome or
antigenome a major nucleocapsid (N) protein, a nucleocapsid
phosphoprotein (P), a large polymerase protein (L), and a RNA
cc antigenome a major nucleocapsid (N) protein, a nucleocapsid
phosphoprotein (P), a large polymerase gene or a te
cc dlasat two attenuating mutations, one of the mutations specifying a
temperature-sensitive (ts) substitution at amino acid Phe521,
least two attenuating mutations, one of the mutations specifying a
temperature sensitive (ts) substitution at amino acid phe521,
least two attenuating mutations, one of the mutations specifying a
temperature sensitive (ts) substitution at amino acid gene MC
C claimed are: (1) an isolated infectious RSV particle which
cc comprises a recombinant RSV (anti)/genome, N), P, and L proteins, a
comprises a recombinant RSV (anti)/genome, N), P, and L proteins, a
c ais-acting regulatory sequence; not a SH, NSI, NS2 or G gene or
c c acis-acting regulatory sequence; or by a change in sequence,
the selected gene; (2) an expression of a SH, NSI, NS2 or G gene
cc c acis-acting regulatory sequence; or by a change in sequence,
the selected from opts RSV 248 (ATCC WR 2450), opts 248/404 (ATCC WR
CC 2454), cpts 248/955 (ATCC WR 2451) or cpts 530/1009 (ATCC WR 2451) or cpts 530/1009 (ATCC WR 2451) or cpts 530/1009 (ATCC WR 2542) or settenuated recombinant RSV and RSV particles are used in a vaccine
cc attenuated recombinant RSV and RSV particles are used in a vaccine
cc attenuated recombinant RSV and RSV particles are used in a vaccine
cc protection against RSV. The expression vector of (2) is used for
the production of infectious attenuated RSV particles.

Query Match 48.0%; Score 441.4; DB 19; Length 15225; Best Local Similarity 68.1%; Pred. No. 3.8e-96; Matches 629; Conservative 0; Mismatches 291; Indels 3; Gaps 1;

4863 CATAATATTCATCATCTCTGCCAATCACAAGTTACACAACGACGGTCACAGTTCAAAC 4922 recaaccargrecaaacacaaaaarcaacecacacacaacacreragaaaaaccereesa 4742 1743 TACTCTCAATCATCTAATTGTAATATCCTCTTTATACAGATTAAATTTAAAATCTAT 4802 1923 AATAAAAACCACACACAGAAAAAACATCACCACCTACCTTACTCAAGTCCCACCAGAAAG 4982 180 181 CATCATATTCATAGCCTCGGCAAACCACAAGTCACACTAACAACTGCAATCATACAAGA 240 301 AATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAGCTTCAAC 360 361 AACACCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAACACAACAAC 420 481 ACCCAATAATGATTTTCACTTCGAAGTGTTTAACTTTTGTACCCTGCAGCATATGCAGCAA 540 CACTCTCAATCATTATTATTCATATCATCGGGCTTATATAAAGTTAAAATCTTAAATCTGT 120 9 TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGA 121 AGCACAAATCACATTATCCATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGC ò ð a 셤 요 ద ð 셤 ઠે ద 셤 ઠે ઠે ઠે ò

5163 ACCAAAAGATGATTACCATTTTGAAGTGTTCAACTTCGTTCCCTGTAGTATATGTGGGAA 5222

Search completed: October 29, 2003, 22:09:33 Job time : 316.982 seca

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GenCore version 5.1.6
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SUMMARIES

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| | ın v | 62 | 200 | | | AR122885 | AR122885 Sequence |
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HRSVGL16 922 bp RNA linear VRL 05-JUN-1997 Human respiratory syncytial virus (MON-7-91) subgroup A, G gene for glycoprotein.
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J. Virol. 68 (9), 5448-5459 (1994)
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Submitted (10-MAY-1994) Dopazo J., Centro Nacional de Biotecnologia
- CSIC, BioInformatica, Universidad Autonoma, Cantoblanco, Madrid,
SPAIN, 28049
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G gene; glycoprotein.
Human respiratory syncytial virus
Human respiratory syncytial virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxovitidae; Pneumovirinae; Pneumovirus.
1 (bases 1 to 922)
Garcia,O., Martin,M., Dopazo,J., Arbiza,J., Fabrasile,S., Jachala, W., Perez-Brena,P., Martinez,I., Garcia-Barreno,B.
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NLSRITSGTTTILASANHKVTHTTAINIOPARGIKNTPTYTHOROPOLGISFS
NLSRITSGTTTILASTTPGYKGNLQPTYKKNTTTTTQTQSSKPTTKGRONKPPNKPN
NDFHFEVFNFVPFYRGTERPTINTTKKNITTTLINNTTGNPKLFSQMETFHSTSSEGNLSP
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                                                                                                                                                                                                                                                                                                                                   Frame shift mutations as a novel mechanism for the generation of neutralization resistant mutants of human respiratory syncytial
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Melero, J.A.
                                                                                                                                                                                                              g protein.
Human respiratory syncytial virus
Human respiratory syncytial virus
Viruses; ssRWA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Pred. No. 1.9e-190;
0; Mismatches 2; Indels 0;

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'organism="Human respiratory syncytial virus"

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TTKDREVPTYKPTERPTINTTKTNITTLINNTTGNPKLTSQMETFHSTSSEGNLSP
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Human respiratory syncytial virus (subgroup A) attachment protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al source text: Human respiratory synctial virus (subgroup Long), cDNA to viral RNA, clones pLF63, pLB69, and pA3. act 5' end of Long G mRNA was not determined.

Location/Qualifiers
                                CACCAAAACAAACATCACAACTACACTGCTCACCAACAACAACCAGGAAATCCAAAAACT
                                                                                                                                                  CACAAGTCAAATGGAAACCTTCCACTCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCA
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Human respiratory syncytial virus

Human respiratory syncytial virus

Human respiratory syncytial virus

Human respiratory syncytial virus

Viruses, ssRNA negative-strand viruses; Mononegavirales;

Paramyxoviridae; Pneumovirinae; Pneumovirus.

Johason, P.R., Spriggs, M.K., Olmsted, R.A. and Collins, P.L.

Johnson, P.R., Spriggs, M.K., Olmsted, R.A. and Collins, P.L.

The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between antigenically related proteins

antigenically related proteins

Proc. Natl. Acad. Sci. U.S.A. 84 (16), 5625-5629 (1987)
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Pred. No. 3.3e-188;
0; Mismatches 4; Indels 0;
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/mol_type="genomic RNA"
/db_xref="taxon:11250"
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/note="attachement glycoprotein
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Matches 904; Conservative
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/tanslation="isknopyraticetymptlnytleissglyklniksiagitles
/tanslation="isknopyraticetymptlnytleissglyktholegists
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NLSBIISQTTIILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTKQRQNKPDNKPN
NTSBIISQTTIILASTTPGVKSNLQPTTVKTNNTTTTQTQPSKPTKQRQNKPDNKPN
NTKPKSVPTYKPTEBPINNTYKTNITTTLINNTTGNPKLTSQMETFHSTSSEGNLSP
SQVSTTSEHPSQPSSPPNTTRQ"
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/organism="Human respiratory syncytial virus"
/mol_type="genomic RNA"
/strain="subgroup A"
/isolate="MON 7 91 (Montevideo/Uruguay, 1991)"
/cell line="HEp-2"
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Pred. No. 7.1e-190;
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/codon start=1
/product="glycoprotein"
/protein id="CAA83872.1"
/db_xref="G1:485889"
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100.0%; Pred. No. 1.6e-186;
ive 0; Mismatches 0;
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Patent: US 5968776-A 28 19-OCT-1999;
Location/Qualifiers
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                          /organism="unknown"
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Best Local Similarity 100.
Matches 894; Conservative
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Unclass 1 to 894)
Klein, W.H., Du, R.-P. and Ewasyshyn, W.E.
Multimeric hybrid gene encoding a chimeric protein which confers
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480

547 540 607 900 667 999 727

787 780 847 840

DNA

AR080424 894 bp Sequence 28 from patent US 5968776. AR080424.1 GI:10007159

RESULT 12
AR080424
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Unknown. Unknown

REFERENCE AUTHORS TITLE

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Innear VRL 29-NOV-2000
structural protein (1C),
leocapaid (N), phosphoprotein
ein (F) and
e, complete cds.
12.7 M11244 M11487 M11505
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tial virus
7683-7687 (1984)
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irus.
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db xref="GI:333927"
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Collins.P.L. Dickens.L.B., Buckler-White,A., Olmsted,R.A., Spriggs,M.K., Camargo,B. and Coelingh,K.V.
Nucleotide sequences for the gene junctions of human respiratory syncytial virus reveal distinctive features of intergenic structure
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Respiratory syncytial virus is a negative-strand RNA pleomorphic enveloped virus of the genemovirus. The matrix protein has no homology with the matrix proteins of other negative-stranded RNA viruses, implying that RS virus has undergone extensive evolutionary divergence. Two unidentified reading frames which potentially encode proteins were located: one overlaps the matrix protein and the other the F protein. The biological significance of these two reading frames is not clear. The positive strand is
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Collins, P.L. and Wertz, G.W.
Nucleotide sequences of the 1B and 1C nonstructural protein mRNAs
Of human respiratory syncytial virus
Virology 143 (2), 442-451 (1985)
86045905
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Proc. Natl. Acad. Sci. U.S.A. 82 (12), 4075-4079 (1985)
85216636
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                                                                                              Respiratory syncytial virus fusion glycoprotein: nucleotide sequence of mRMs, identification of clasavage activation site and amino acid sequence of N-terminus of F1 subunit Nucleic Acids Res. 13 (5), 1559-1574 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of the G protein gene of human respiratory
                      (bases 5602 to 7423)
Elango, N., Satake, M., Coligan, J.E., Norrby, E., Camargo, E. and
Venkatesan, S.
                                                                                                                                                                                                                                                                                                                                                                                                            9 (bases 4627 to 5544)
Wertz,G.W., Collins,P.L., Huang,Y., Gruber,C., Levine,S. and
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Collins, P.L. and Wertz, G.W.
The 1A protein gene of human respiratory syncytial virus:
nucleotide sequence of the mRNA and a related polycistronic
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Collins, P.L., Anderson, K., Langer, S.J. and Wertz, G.W.
Correct sequence for the major nucleocapsid protein mRNA (
respiratory syncytial virus
Virology 146 (1), 69-77 (1985)
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                            TGCAAACATGTCCAAAAACAAGGACCAACGCACCGCTAAGACACTAGAAAAGACCTGGGA
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Best Local Similarity 95.5%; Pred. No. 1.2e-177;
Matches 878; Conservative 0; Mismatches 41; Indels
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            Unknown.
Unclassified.
1 (bases 1 to 15222)
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1 Torrence,P.F., Silverman,R.Hugh., Cirino,N.Mario., Li,G. and Xiao,W.
RName L activators and antisense oligonucleotides effective treat RSV infections
Patent: Us 5998602A 23 07-DEC-1999;
Location/Qualifiers
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MEDLINE=91065351; PubMed=2249671;
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MEDLINE=91065351; PubMed=2249671;
MACACIAL Barreno B., Portela A., Deblgado T., Lopez J.A., Melero J.A.;
T. "Frame shift mutations as a novel mechanism for the generation of newtralization resistant mutants of human respiratory syncytial
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                                181 TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTBEPTINTTK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";

J. Virol. 68:548-5458(1994).

EMBL; Z33429; CAA83872.1; -.

InterPro: IPR000925; Glycoprote G.

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PROSTIE: PS000812; PHOSPHOPANTETHEINE; 1.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycoptotin (Fregment).
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Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A., Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J., Pringle C.R.;
Pringle C.R.;
"Identification of mutations contributing to the reduced virulence a modified strain of respiratory syncytial virus.";
Vaccine 14:1637-1646(1956).
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Baston A.J.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U39662; AAC57026.1;
InterPro; IPR000925; Glycoprot G.
InterPro; IPR006162; Ppantne attach.
Pfam; PF00802; Glycoprotein G.T.
PROSITE; PRO0012; PHOSPHOPANTETHINE; I.
SEQUENCE 298 AA; 32749 MW; 60F27B299497F31 CRC64;
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viruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
vCBI_TaxID=11250;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
04, Created)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein (G).
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Attachment protein (G).
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Best Local Similarity 90.2
Matches 268; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SVKSTLQSTTVKTKNTTTTKIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
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MEDLINE=99022964; PubMed=9806017;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
T. "Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
to infections in children.";
J. Infect. Dis. 178.925-33.

R EMBL; AF065405; AAD02941.1;
R EMBL; AF065405; AAD02941.1;
R InterPro; IPR006162; Pantne attach.
R Ffam; PF00802; Glycoprotein G; 1.
R PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 297 AA; 32572 MW; 5C10E719A05EF5C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKNKDQRTTKTLEKTWDTLAHLLFISSCLYKLALKSIAQITLSILAMIISTSLIIAAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFSNLSETTSQTTTILASTTP
                                                                                                             "Identification of mutations contributing to the reduced virulence of a modified strain of respiratory syncytial virus."; Vaccine 14:1637-1646(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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                          Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A., Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J., Pringle C.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 298;
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                                                                                                                                                                                                                                                STEATHS 2 tell;
Baston A.J.;
Baston A.J.;
Baston A.J.;
Submitted (CCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U39661; AACS7036.1; -.
InterPro; IPR000925; Glycoprot G.
InterPro; IPR006162; Pabatine attach.
Pfan; PF00802; Glycoprotein G; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 298 AA; 32779 WW; 67FAA043682FAA50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Human receiver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 1389; DB 12; 90.9%; Pred. No. 8.4e-95; ive 7; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1365;
MEDLINE=97185152; PubMed=9032893;
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Best Local Similarity 90.9
Matches 271; Conservative
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                                                                                                                              1 MSKNKDORTAKTLERTWDTLNHLLFISSCLYKLNLKSVAQITLSILAMIISTSLIIAAII
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                                                                              1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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"Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";

J. Virol. 68:548-5458[1944].

EMBL; 233427; CAA83870.1; -.
InterPro; IPR000925; Glycoprot G.
InterPro; IPR000825; Pantne attach.

Ffam; PF00802; Glycoprot G.

Pfam; PF00802; Glycoprot G.

Pfam; PR00802; Glycoprot G.

Pfam; PR00802; Glycoprot G.

PROSITE; PS00012; PAOSPHOPANTETHEINE; 1.

RROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
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MEDLINE=94335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4.9e-93;
ches 21;
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89.9%; Pred. No. 5.8e-93;
iive 10; Mismatches 20;
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                              Mismatches
  90.2%; Pred. No.
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Best Local Similarity 89.99
Matches 267; Conservative
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181 TCWAICKRIPNKKPGKRTTTKPTKKPTLKTTKKDPKPQTTKSKEAPTTKPTEEPTINTTK 240
ESCUENCE FROM N.A.

STRAIN=Bubgroup A;

KEDLINE=94335057; PubMed=8057427;

MEDLINE=94335057; PubMed=8057427;

MEDLINE=94335057; PubMed=8057427;

A darcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,

A darcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,

A darcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,

A hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,

Melero J.A.,

A) cocirculating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";

C J. Virol. 68:5448-5455(1994).

E MBL, Z33422, CAA83875.1.

E MBL, Z33422, CAA83875.1.

E MBL, Z33422, CAA83875.1.

E MBL, Z33422, CAA83875.1.

R InterPro; IPRO00225; Glycoprot G.

Pram, PRO0812; PROSECTEIN G; I.

PROMITE, PROMO12; PHOSPHOPANTETHEINE; I.

S REQUENCE 297 AA; 32581 MW; AD947B2318193306 CRC64;
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89.2%; Pred. No. 3.2e-92;
ive 10; Mismatches 22; Indels 0;
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Matches 265; Conservative
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Q1-NOV-1996 (
Q1-NOV-1996 (
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         181 TCWAICKRIPNKKPGKRTTTKPTKKPTLKTTKKDPKPQTTKSKEVPTTKPTEEPTINTTK 240
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                                                  241 TNITTLLINNTTGNPKLISQMETPHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTR 297
                                                                           241 TNIITTLITSNITRNPELISQMETFHSTSSEGNPSPSQVSITSEYPSQPSSPPNTSR 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.; Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.; "Antigenic and genetic diversity among the attachment proteins of group A respiratory syncytial viruses that have caused repeat infections in children."; J. Infect. Dis. 178:925-932(1998).

BWBL; ARCOSG406; AAD02942-11. -
InterPro; IPR000925; Glycoprot. G.
InterPro; IPR000162; Ppantne attach.
PROSTIE; PS00012; Pycoprotein G; 1.
PROSTIE; PS00012; PS0PROPROPANTETHEINE; 1.
SEQUENCE 298 AA, 32781 MW; ARTC9E05547C5745 CRC64;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                                                                                                                                                                                                                                                                                                  Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein G.
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Last annotation update)
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88.9%; Pred. No. 2.3e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.9%; Pred. No. 2.3e-
Matches 265; Conservative 10; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
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                                                                                                                                                                                                         PRELIMINARY;
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Q9YVB4
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241 TNITTTPLTSNTTRNPELTSQMETFHSTSSEGNPSPSQFSITSEYPSQPSPPNTSR 297
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Changes in the G glycoprotein.";

WHEL: Z33428; CAR83871.1; -.

InterPro; IPR000925; Glycoprot_G.

InterPro; IPR00652; Ppantne attach.

PROSTE; PS00012; PHOSEPHORATETHEINE; 1.

SRQUENCE 297 AA; 32555 MM; 9D0A69BECAEGBGC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDALINE-94335057, PubMed-8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; sBRNA negative strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SSSS SEEPERS SSS

240 240

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61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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INITITILINNITIGNPKLISOMETFHSISSEGNLSPSQVSITSEHPSQPSSPPNTTR 297
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                                                                                                                                                                  1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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A and B Strains
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-MAX-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2003 (TrEMBLrel. 2), Last annotation update)
Attachment glycoprotein G (Fragment)
Human respiratory syncytial virus.
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88.2%; Pred. No. 4.1e-91;
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MEDLINE=94335057; PubMed=8057427;

Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,

Hortal M., Perez Brena P., Martinez I., Garcia-Barreno B.,

Melero J.A.;

Melero J.A.;

"Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic Changes in the G glycoprotein.";

J. Virol. 68:5449-5459(1994).

REMBL; Z33456; CAA83879.1; -

REMBL; Z33456; CAA83879.1; -

REMBL; Z33456; CAA83879.1; -

REMBL; Z33456; CAA83879.1; -

REMBL; Z33456; CAA83870.1; -

REMBL; REPPO; IPRO06162; Ppantne attach.

Refam; PP00802; Glycoprotein G; 1.

REMBL; REPPO; REMONIC STRUENES; REMBL; REMONIC STRUENES; REMBL; REM
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                                                                                                                                                                                      MSKNKDQRTAKTLEKTWDTLNHLLPISSGLYKLNLKSVAQITLSILAMIISTSLITAII
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                             Length 297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                                                         Indels
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                             DB 12;
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                   87.1%; Score 1345; DB 12
88.9%; Pred. No. 1.5e-91;
ive 10; Mismatches 23
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                                                                                  264; Conservative
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les 262; Conservative
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01-MAR-2003
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                          Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.,
"Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
infections in children."

J. Infect. Dis. 178:225-932(1998).

EMBL, AF065407; AAD02943.1; -.

Enterpro, IRR000925; Glycoprot G.

Interpro, IRR000162; Phantne attach.

Pfam; PF00802; Glycoprotein G; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 TLLINNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 293;
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Viruses; sRRNA negative-strand viruses; Mononegavirales;
Paramexycoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=1814;
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Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
SMBL). 2. CAA51764.1; -.
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR00612; Papatine attach.
Pfam. PF00802; Glycoprotein G; 1.
PROSSITE; PS00012; PROSPHOPANITETHRINE; 1.
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Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment
subgroup A respiatory syncytial vuruses.";
J. Gen. Virol. 72:2091-2096(1991).
                                                                                                                                                                                                                                                                                                                                                                   293 AA; 32125 MW; 17B5B43396A63CCF CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
G protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                Score 1336; DB 12;
Pred. No. 6.6e-91;
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                                                                      STRAIN=WV6973;
MEDLINE=99022964; PubMed=9806017;
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Best Local Similarity 90.1%;
Matches 264; Conservative
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Best Local Similarity
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                                               SEQUENCE FROM N.A.
    NCBI_TaxID=11250;
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MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
Identification of variable domains of the attachment (G) protein subgroup A respiatory syncytial vuruses.";
J. Gen. Virol. 72:2091-2096(1991).
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Respiratory syncytial virus.
Viruses, BRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=12814;
                                                                               Length
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Cane P.A.;
Cane P.A.;
Cane P.A.;
Cane P.A.;
Cane P.A.;
InterPro 1 PR000925; Glycoprot G.
InterPro; IPR00162; Papatte attach.
Pfam; PF00802; Glycoprotein G.
Prosite; PR00012; PR000162; Papatte attach.
Pfam; PF00802; Glycoprotein G.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
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1 1
295 AA; 32490 MW; 48D835F670FF8006 CRC64;
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                                                                            DB 12;
                                                                         Query Match 86.4%; Score 1334; DB 12
Best Local Similarity 88.4%; Pred. No. 9.4e-91;
Matches 260; Conservative 8; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 AA
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SEQUENCE FROM N.A.

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STRAIN=subgroup A;

Marbines 4313567; PubMed=8057427;

A Gazcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,

A Hortal M., Perez Brena P., Martinez I., Garcia-Barreno B.,

A Hortal M., Perez Brena P., Martinez I., Garcia-Barreno B.,

A Hortal M., Perez Brena P., Martinez I., Garcia-Barreno B.,

A Hortal M., Perez Brena P., Martinez I., Garcia-Barreno B.,

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A Hortal M., Perez Brena P., Martinez I.,

DR InterPro; IPRO06152; Papathe attach.

BR PEGNITE; PS00012; PHOSPHOPANTETHEINE; I.

SEQUENCE 298 AA; 32729 MW, 4E890FFD43845744 CRC64;
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   KSNLOPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDPHFEVPNFVPCSICSNNPTC
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86.4%; Score 1334; DB 12; Length 298;
Best Local Similarity 88.2%; Pred. No. 9.5e-91;
Matches 261; Conservative 10; Mismatches 25; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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Search completed: October 29, 2003, 17:40:52 Job time : 75.283 sec8

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2003, 17:12:25; Search time 16.3057 Seconds (without alignments) 859.454 Million cell updates/sec Run on:

US-09-462-816-2 1544 1 MSKXKDQRTAKTLEKTWDTL.....VSTTSEHPSQPSSPPNTTRQ 298 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

| | Description | P20895 human respi | human | human | human | human | human | human | P27021 human respi | human | human | bovine | bovine | bovine | bovine | bovine | O10686 bovine resp | ovine r | bovin | bovine | bovine | drosop | Q9y493 homo sapien | | | | P13729 drosophila | P57999 oryctolagus | Q9hc84 homo sapien | _ | - | P13728 drosophila | | - |
|-----------|-----------------------|--------------------|------------|------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|--------------------|-----------|------------|------------|------------|------------|--------------------|------|------------|------------|-------------------|--------------------|--------------------|------------|---------|-------------------|----------|-----------|
| SUMMARIES | ID | VGLG HRSVL | VGLG_HRSVA | VGLG HRSV3 | VGLG_HRSV6 | VGLG_HRSV7 | VGLG_HRSV4 | VGLG_HRSV5 | VGLG_HRSV2 | VGLG_HRSV8 | VGLG_HRSV1 | VGLG_BRSV1 | VGLG_BRSV4 | VGLG_BRSVC | VGLG BRSV2 | VGLG BRSVW | VGLG BRSVS | VGLGORSVW | VGLG_BRSV7 | VGLG_BRSVL | VGLG_BRSVR | SGS3_DROME | ZAN HUMAN | | MUC2_HUMAN | DAN4_YEAST | SGS3_DROSI | ZAN RABIT | MUSB_HUMAN | AMYH YEAST | ZAN PIG | SGS3 DROYA | VGP3 EBV | ZAN MOUSE |
| | DB : | М | Н | Н | Н | П | Н | ۳Ħ | н | н | - | н | н | н | | Н | | | - | - | -1 | - | 1 | - | Н | | | | | - | - | - | Н | ч |
| | Query Match Length | ; | 298 | 297 | 297 | 297 | 297 | 298 | 297 | 292 | 292 | 263 | 263 | 257 | 263 | 263 | 257 | 263 | 257 | 257 | 257 | 307 | 2812 | 662 | 5179 | 1161 | 217 | 2282 | 5703 | 1367 | 2476 | ø | 907 | 7 |
| dę | Query | 0 | 91.8 | ~ | ~ | φ | S | S | 84.7 | O | თ ≀ | 0 | | 19.4 | | 19.1 | 18.5 | | 18.1 | 17.5 | 17.3 | 13.5 | 12.9 | 12.6 | 12.5 | 12.4 | 11.9 | 11.1 | 11.0 | 11.0 | 10.7 | 10.4 | 10.3 | 10.2 |
| | Score | 1530 | 1418 | 1343 | 1343 | 1328 | 1324 | 1313 | 1307 | 767.5 | 761 | 309.5 | 308.5 | 299 | 295.5 | 294.5 | 285 | 284 | 279 | 270 | 267 | \sim | 198.5 | 194 | 193 | 191 | 183 | 171.5 | 170 | 169.5 | 164.5 | 160 | 159.5 | 57. |
| | Result No. | H | 7 | m | 4 | M. | 9 | 7 | ∞ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 50 | 21 | 22 | 23 | 24 | 25 | 26 | 7.7 | 28 | 29 | 30 | 31 | 32 | 33 |

| P28968 equine herp Q07284 epstein-bar P46590 candida alb Q09624 caenorhabdi P98088 homo sapien Q62635 rattus norv P54197 coccidioide Q01836 listeria in Q13854 schizosacch P38894 saccharomyc P39712 saccharomyc P39712 saccharomyc P38739 saccharomyc |
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| VGLX HSVEB VGP3 EBVAB ALS1 CANAL YS89 CAEEL MUZA HUWAN MUCZ RAT CHIZ COCPO PEO LISIN YFGG SCHPO FLOS YEAST YAG3 YEAST |
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ALIGNMENTS

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Query Match Best Local Similarity 99.0%; Pred. No. 8.6e-93; Matches 295; Conservative 1; Mismatches 2; Indels

us-09-462-816-2.rsp

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120
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SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95266253; PubMed=7747420, Connors M., Cove U.B. Jr., Firestone C.Y., Murphy B.R., Collins P.L.; A cold-passaged, attenuated strain of human respiratory syncytial virus contains mutations in the F and L genes.";
                       1 MSKNKDQRTAKTLEKTWDTLAHLLPISSGLYKLANLKSIAQITLSILAMIISTSLITAII
MSKNKDQRTAKTLEKTWDTLNHLLF1SSGLYKLNLKSVAQ1TLS1LAM11STSL11TAI1
                                                                                FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-85216636; PubMed-3858865; Wettz G.W. Levine S., Ball L.A.; Wettz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.; "Nucleotide sequence of the G protein gene of human respiratory syncytial virus reveals an unusual type of viral membrane protein."; Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
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MEDLINE=86067198; PubMed=4069997;
Satake M., Coligan J.E., Elango N., Norrby E., Venkatesan S.;
"Respiratory syncytial virus envelope glycoprotein (G) has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human respiratory syncytial virus (strain A2).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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135 135 N-LINKED (GLCNAC. .) (POTENTIAL)
231 237 N-LINKED (GLCNAC. .) (POTENTIAL)
251 251 N-LINKED (GLCNAC. .) (POTENTIAL)
258 AA; 32586 MW; 993C3D2DD68BCG34 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
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                                                                                                                                                                                                                                                                                   EMBL, X03149; CAA26928.1; -. EMBL, U50362; AAB86663.1; -. EMBL, U50363; AAB86675.1; -. EMBL, U63644; AAC55969.1; -.
                                                                                                                                                                                                                                                           EMBL; M11486; AAB59857.1; -.
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DOMAIN
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VGLG_HRSV7
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MEDLINE=91374005; PubMed=1895054;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

"Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";

J. Gen. Virol. 72:2091-2096(1991).

-I- FUNCTION: UNLIKE THE OTHER PARAMXXVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ATTIVITIES.

-I- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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                                                                                                                                                                                                                                                                                                                                                                                    1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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HEMAGGLUTINATING ACTIVITIES.

-!- SUBGELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INPECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIKIONS.

-!- PTM: MAY CARRY 40-480 SEPRANTE O-LINKED CAREDOHURARE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                297 EXTENCELLULAR (POTENTIAL).
135 N-LINKED (GLCNAC. .) (POTENTIAL).
237 N-LINKED (GLCNAC. .) (POTENTIAL).
2551 N-LINKED (GLCNAC. .) (POTENTIAL).
32525 MW, 48448F9E091E1802 CRC64;
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                                                                                                                                                                                                                                                                                                               87.0%; Score 1343; DB 1; Length 297; 88.6%; Pred. No. 1.2e-80;
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus (strain rsb6256).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11256;
                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
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11; Mismatches
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                                                                                                                                                                                    POTENTIAL.
                                                                                      PIR, JQ1205, JQ1205.
InterPro, IPR000925, Glycoprot G.
Pfam; PF00802, Glycoprotein G; I.
Transmembrane, Glycoprotein.
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; Transmembrane; Glycoprotein.
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tes 263; Conserv
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VGLG_HRSV6
ID VGLG_HRSV6
AC P27025;
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TRANSMEM
DOMAIN
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CARBOHYD
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J. Gen. Vitol. 72:201-205(1991).

-I - FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEARAGGIUTINATING ACTIVITIES.

-I - SUBCELLIOLAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MENGRANE OF THE VIRIONS.

-I - PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of
                                EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                          Score 1343; DB 1; Length 297;
Pred. No. 1.2e-80;
8; Mismatches 26; Indels C
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human respiratory syncytial virus (strain rsb6614).
Viruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                     6781756C38B64A80 CRC64;
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 CYTOPLASMIC (POTENTIAL).
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THGEFPO: TRR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
                                                                                                                                                                          87.0%;
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Best Local Similarity 88.5
Matches 262; Conservative
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Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of "Identification of variable domains of the attachment (G) protein of "Identification of variable domains of the attachment (G) protein of "Identification of variable domains of the attachment (G) protein of "Identification of variable domains of the attachment (G) protein of "Identification of variable domains of the attachment (G) protein of "Identification of variable domains of the attachment (G) protein of "Identification of variable domains of protein of "Identification of variable domains" in the province of variable domains of variable of "Identification" of variable domains of large protein of "Identification" of variable domains of large protein of "Identification" of variable domains of large protein of "Identification" of variable domains of 
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                                                                                                                                Gaps
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EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
294 294 N-LINKED (GLCNAC. . .) (POTENTIAL) 297 AA; 32670 MW; 58B384028E437ACD CRC64;
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                                                                          Length 297;
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                                                                                                                             29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory syncytial virus (strain rsb5857).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
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                                                                     Query Match 86.0%; Score 1328; DB 1; Best Local Similarity 87.8%; Pred. No. 1.1e-79; Matches 260; Conservative 7; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1324; DB 1
Pred, No. 2e-79;
7; Mismatches 2
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297 AA;
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Matches 260;
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P27023;
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J. Gen. Virol. 72:2091-2096(1991).

-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-!- FTM: MAY CARRY 40-80 SERRARD O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
1 MSKTKDQRTAKTLERTWDTLAHLLFISSCLYKLNLKSIAQITLSILAMISTSLIIAAII
                                                                                                                                                                                  GVKSNLOPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFRVPCSICSNNP
                                                                                                                                                                                                                                                                                                                           1 MSKTKDQRTAKTLEKTWDTLAHLLFISSCLYKLALKSIAQITLSILAMIISTSLIIAAII
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                                                                        61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory syncytial virus (strain rsb6190).
Viruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID=11255;
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N-LINKED (GLCNAC. .) (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEDLINE=91374005; PubMed=1895054; Cane P.A., Matthews D.A., Pringle C.R.; Identification of variable domains of the attachment
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%; Pred. No. 1.1e-78;
11; Mismatches 28;
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SVESILGSTIVKTIKNTITIQIQPSKPITKQRQNKPPNKPNNDFHFFVFVFVFCSICSNNP 180
                                                                                                                      GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                    TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
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PIASANNKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFFNLSGTTSQTTAILALTTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subgroup A respiratory syncytial viruses..;
J. Gen. Virol. 72:2091-2096(1991).

-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTRINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTRIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INPECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- FTM: MAX CARRY 40-80 SEPRARE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                            Human respiratory syncytial virus (strain rsb642)
                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                            297 AA.
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                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=91374005; PubMed=1895054;
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InterPro. 1PR000925, Glycoprot. G. Pfam, PF00802; Glycoprotein. G; 1. Transmembrane; Glycoprotein.
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86.58;
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DOMAIN
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P27021;
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VGLG_HRSV2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91374595; PubMed=1895391; Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.; J. Virol. 65:5425-5434(1991).

-! FUNCTION. UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL, VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
-! SUBCELLULAR LOCATION: EXPRESSED ON THE SURRACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEDNATE O-LINKED CARBOHYDRATE CHINS DISTRIBUTED AMONG THE 91 SERINB AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKHKNQRTASTLEKTWDTLANHLIVISSCLYRLANLKSIAQIALSVLAMIISTSLIIAAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                 Sullender W.M., Anderson K., Wertz G.W.;
"The respiratory syncytial virus subgroup B attachment glycoprotein:
analysis of sequence, expression from a recombinant vector, and
evaluation as an immunogen against homologous and heterologous
subgroup virus challenge.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                 241 TNIITTPLTSNTARNPELTSQMETFHSTSSEGNPSPSQVSITSEYPPQPSSPPNTPR
241 INITITILINNITGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTR
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N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . . ) (POTENTIAL)
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                                                                                                                                                                                                                                                         Human respiratory syncytial virus (subgroup B / strain 8/60).
                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-MUG-1992 (Rel. 23, Last amnotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI TaxID=11258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BECGOC8SEPOS7BBS CRC64;
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                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90357765; PubMed=1697126;
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Transmembrane; Glycoprotein.
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66 PC
292 E3
81 N-
100 N-
32143 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subgroup virus challenge."
Virology 178:195-203(1990)
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                                                                                                                              STANDARD;
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81 86
86 100 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                      VGLG HRSV8
P23041;
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TRANSMEM
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SEQUENCE
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61 FIISANHKVTLTTVTVQTIKNHTEKNISTYLTQVPPERVNSSKQPTTTSPIHTNSATISP 120

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1 MSKHKNQRTARTLEKTWDTLNHLIVISSCLYRLNLKSIAQIALSVLAMIISTSLIIAAII PIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISPSNLSELTSQTTTILASTTP 121 GVKSNLOPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP

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                                                                                                                                              180
                                                                                                                                                                                                                                                                                         239
                                                                                                                                                                                                                                                                                                                               181 LCKSICKTIDSNXPKKKPTIKPTNKPTTKTTNKRDPKTPAKMPKKEIITNPTKKPTKKT 240
                                                                   61 FIISANHKVTLTTVTVOOTIKNHTGKNISTVLTOVPPERVNSSKOPTTISPIHTNSATISP 120
                                                                                                                                                                                                                  121 NTKSETHHTTAQTKGRITTSTQTNKPSTKSRSKNPPKKPKODYHFEVPNFVPCSICGNNQ 180
FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87289657; PubMed=2441388;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;

"The G Blycoprotein of human respiratory syncytial viruses of
subgroups A and B: extensive sequence divergence between
antigenically related proteins.";
Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).

-!- FUNCTION: UNLIKE THE OTHER PARAMIXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                         TCWAICKRIPNKKPGKKTTTKPTKKPTFKTT-KKOLKPQTTKPKEVPTTKPTEEPTINTT
                                                                                                                                                  GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS. AND INCORPORATED IN THE MEMBRANG OF THE VIRIONS.
PTM: MAY CARRY 40-60 SEPARTE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                        240 KTNITTILITNNTTGNPKLISQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSP 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 BRDISTSQSTVIDIITPKYTIQQQSLHSTTSBNTPSSTQ1PTASB-PS-TSNP 291
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86 86 N-LINKED (GLCNAC. . .) (POTENTIAL)
100 N-LINKED (GLCNAC. . .) (POTENTIAL)
292 AA, 32306 MW, BC8CS9F69CA7AFC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus (subgroup B / strain 18537).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEE-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; 1.
Transmembrane; Glycoprotein.
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292
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                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ology 211:48-18(1997).

FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE FUNCTION: UNLIKE THE OTHER PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

SUBCELLULAR LOCATION: EXPRESSED ON THE SURPACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
                     181 LCKSICKTIPSNKPKKKPTIKPTNKPTTKTTNKRDPKTPAKMPKKEIITNPAKKPTLKTT
181 TCWAICKRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPOTTKPKEVPTTKPTEEPTINTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97288324; PubMed=9143302;
Furze J., Roberts S., Wertz G., Taylor G.;
"Antigenically distinct G glycoproteins of BRSV strains share a high degree of genetic homogeneity.";
Virology 231:48-58(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                       240 KTNITTLLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPS 287
                                                                                           241 BRDTSISQSTVLDTITPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 POTENTIAL.
186 EXTRACELLULAR (POTENTIAL).
187 BY SIMILARITY.
127 N-LINKED (GLCNAC. .) (POTE
163 N-LINKED (GLCNAC. .) (POTE
251 N-LINKED (GLCNAC. .) (POTE
251 N-LINKED (GLCNAC. .) (POTE
251 N-LINKED (GLCNAC. .) (POTE
                                                                                                                                                                                                                           15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                      Viruses; sgRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                                                     Sovine respiratory syncytial virus (strain 127)
                                                                                                                                                                                              263
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                                                                                                                                                                                            STANDARD;
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176
127
163
251
263 AA;
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                                                                                                                                                                                            VGLG BRSV1
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Matches
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Matches 158; Conservative

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Similarity

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                   FIASANHKVILITAIIQDAISQIKNTIPTYLIQDPQLGISFSNLSRIISQTTIILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bloinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                         GVKSNLQPITVKTKNTTTTQTQPSK---PITKQRQNKPPNKP-----NNDFH--FEVF 168
                                                                                                                                                                                                                                         169 PHVPCSTCEGNPACSPLCQIELERAPSSAPTITLKKAPKPKTTKKPTKTTIYHRTSPEAK 228
                                                                                                      61 YISVGNAKAKPISKPITQQTQQLQNHTPPPLTEHNY------KSTHTSIQSTTL 108
                                                                                                                                                                            109 SOPPNIDTISGTIYGHPINRIQNRKIKSQSIPLATRKPPINPLGSNPPENHODHNNSQTL 168
                                      9
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Furze J., Roberts S., Wertz G., Taylor G.;
Virology 231:48-58 (1997).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- SIMILARITY: TO THE G PROTEINS OF BITHER THE SUBGROUP A OR B HRS VIRUS.
                      1 | SONHTHIPKFKTLKRAWKASKYFIVGLSCLYKFNLKSLVQTALTTLAMITLTSLVITAII
                                                                                                                                                                                                               NFVPCSICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLK
 MSKONKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
W, D592D79EF8ES535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine respiratory syncytial virus (strain 4642) (BRS).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                 217 POTTKPKEVPTTKPTEEPTINTTKTNITTLLINNTT 253
                                                                                                                                                                                                                                                                                                         229 LQTKKIMATPQQGILSSP---EHQTNQSTTQISQHTS 262
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263 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                            BRSV4
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                                                                                                                                                                  FIASANHKVTLTTAIIQDAISQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                 121 GVKSNLOPTTVKTKNTTTTQTQPSK---PTTKQRQNKPPNKP-----NNDFH--FEVP 168
                                                                                                                                                                                                           61 YİSVGNAKAKPİSKPITQOLQALINHIPPPLIEHNY------KSTHISIQSİTL 108
                                                                                                                                                                                                                                                                                        109 SQPPNIDTISGTIYGHPINRIQNRKIKSQSIPLATRKPPINPLGSNPPRNHQDHNNSQTL 168
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Biochemistry 35:14684-14688(1996).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
                                                                                                                       1 MSNHTHHPKFKTLKRAWKASKYFIVGLSCLYKFNLKSLVQTALTTLAMITLTSLVITAII
                                                                                                                                                                                                                                                                                                                                                                         169 PHVPCSTCEGNPACSPLCQIBLERAPSSAPTITLKKAPKPKTTKKPTKTTIYHRISPEAK
                                                                                   1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                  169 NFVPCSICSNNPTCWAIC----KRIPN------KKPGKKTTTKPTKKPTFKTTKKDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91012801; PubMed=2214024;
MEDLINE=91012801; Anderson K., Wertz G W.;
Lerch R.A., Anderson K., Wertz G W.;
Nucleotide sequence analysis and expression from recombinant vectors demonstrate that the attachment protein G of bovine respiratory syncytial syncytial virus is distinct from that of human respiratory syncytial
                                                 Gaps
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-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECT CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doreleijers J.F., Langedijk J.P.M., Haard K., Boelens R., Rullmann J.A., Schaaper W.M., van Oirschot J.T., Kaptein R., "Schution structure of the immunodominant region of protein G
        Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BRS)
                                                 Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine respiratory syncytial virus (strain Copenhagen) (Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                          253
                                                                                                                                                                                                                                                                                                                                                                                                                                               229 LQTKKIMVTPQQGILSSP---EHQTNQSTTQISQHTS 262
    20.0%; Score 308.5; DB 1; 32.5%; Pred. No. 1.5e-13; ive 32; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                    217 PQTTKPKEVPTTKPTEEPTINTTKTNITTLTNNTT
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                          Conservative
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                       Similarity
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ID VGLG BRSVW
AC 010687;
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                                                                                                                                                                                                                                                                                             169 NFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTT 228
                                                                                                                                                                                                                            61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                             121 GVKSNLQPITVKTKNTTTTQTQPSK---PTTKQRQNKPPNKPNNDF-------HFEVF 168
                                                                                                                                                                                                                                                                            109 SQLINIDTIRGITYGHSINETONRKIKGQSILPATRKPPINPSGSIPPENHQDHNNFQTL 168
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                                                                                                                                                                                                     1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
                                                                                                                                                          ch 19.4%; Score 299; DB 1; Length 257; 1 Similarity 31.6%; Pred. No. 6e-13; 92; Conservative 33; Mismatches 120; Indels
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine respiratory syncytial virus (strain 220-60) (BRS)
Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                 POTENTIAL. EXTRACELLULAR (POTENTIAL)
                                                                                                                                           28569 MW; OB86D541FBA0657D CRC64;
                                 3D-structure.
CYTOPLASMIC (POTENTIAL)
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                                                                                 N-LINKED
N-LINKED
N-LINKED
       PDB; 1BRV; 05-JUN-97.
InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; I.
Transmembrane; Glycoprotein; 3D-8
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257 AA;
PIR; A36408; MGNZBR
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GVK----SNLOPITVKTKNT-TTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCS
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MEDLINE=97286324; PubMed=9143302;
Furze J., Roberts S., Wertz G., Taylor G.;
"Antigenically distinct G glycoproteins of BRSV strains share a high degree of genetic homogeneity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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tive 35; Mismatches 123; Indels
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263 EXTRACELLULAR (POTENTIAL).
186 BY SIMILARITY.
182 BY SIMILARITY.
127 N-LINKED (GLCNAC. .) (POTE
163 N-LINKED (GLCNAC. .) (POTE
251 N-LINKED (GLCNAC. .) (POTE
251 N-LINKED (GLCNAC. .) (POTE
251 N-LINKED (GLCNAC. .) (POTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Major surface glycoprotein G (Attachment glycoprotein
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15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein_G; I.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                          EMBL; Y11205; CAA72089.1; -. PIR; JQ2284; JQ2284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GVKSNLQPTTVKTKNTT-----TTQTQPSKPTTKQRQNKPPNKP-----NND 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 FH--FEVFNFVPCSICSNNPTCWAICK-----RIP----NKKPCKKTTTKPTKKPTF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 DHNNSQTLPHVPCSTCEGNPACSSLCQIGPERASSRAPTITLKKTPKPKTTKKFTHH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKNKDQRTAKTLEKTWDTLAHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%; Score 294.5; DB 1; Length 263; 30.8%; Pred. No. 1.2e-12; Live 35; Mismatches 102; Indels 63; Gaps
                                                                                                                                                                                                                                                                    66 FOTENTIAL.
186 BY SIMILARITY.
182 BY SIMILARITY.
187 N-LINKED (GLCNAC. .) (POTENTIAL).
187 N-LINKED (GLCNAC. .) (POTENTIAL).
183 N-LINKED (GLCNAC. .) (POTENTIAL).
163 N-LINKED (GLCNAC. .) (POTENTIAL).
163 N-LINKED (GLCNAC. .) (POTENTIAL).
29050 MW; 0D06AF7FCB46B858 CRC64;
SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 KTTKKDLKPQ----TTKPKEVPTTKPTEEPTINTTKTNITTLLTNNTT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 RKTSPEAKPQPKNNTAAPQQGILSSPEHH-----TNQPTTQIQQHTS 262
                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                               EMBL; Y08717; CAA69967.1; -.
HSSP; P22261; IBRV.
InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; I.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 30.89
                                                                                                                                                                                                                                                        37
66
263
186
182
127
163
233
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TRANSMEM
DOMAIN
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DISULFID
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CARBOHYD
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CARBOHYD
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Search completed: October 29, 2003, 17:38:37 Job time : 18.3057 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 29, 2003, 17:33:35; Search time 28.6755 Seconds (without alignments) 999.400 Million cell updates/sec

US-09-462-816-2 Perfect score:

1 MSKNKDQRTAKTLEKTWDTL.......VSTTSEHPSQPSSPPNTTRQ 298 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

| | Description | | surface | ğ | u | G protein - Human | v | | attachment protein | | major surface glyc | | -4 | glycoprotein G - b | major surface glyc | | glycoprotein G - o | glycoprotein G - b | attachment glycopr | salivary glue prot | mucin FIM-C.1 - Af | mucin 2 precursor, | hypothetical prote | probable membrane | apomucin precursor | mucin-like glycopr | larval glue protei | salivary glue prot | microfilarial shea | hypothetical prote |
|-----------|---------------------|--------|---------|--------|--------|-------------------|--------|--------|--------------------|--------|--------------------|--------|------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | aı | MGNZRL | MGNZ | JQ1205 | JQ1208 | JC5680 | JQ1209 | JQ1206 | JQ1207 | JQ1204 | MGNZ60 | MGNZ18 | VHNZ | PQ0768 | MGNZBR | JQ2284 | JQ2388 | PQ0769 | A48732 | GSFF3 | A45155 | A43932 | T22696 | S57180 | A53715 | T31113 | 850125 | S01358 | T46740 | T22808 |
| | DB | - | - | N | N | N | C3 | N | ~ | N | н | П | Н | ~ | Н | 7 | ~ | N | N | - | N | ~ | | | | | | | | 7 |
| | Length | 298 | 298 | 297 | 297 | 298 | 297 | 297 | 298 | 297 | 292 | 292 | 467 | 250 | | | | | | | | m | | - | | | | | | |
| • | % Query Match | 99.1 | 91.8 | 87.0 | 87.0 | 86.3 | 86.0 | 85.8 | 85.0 | 84.7 | 49.7 | 49.3 | 27.5 | 19.4 | 19.4 | 19.1 | 18.4 | 18.1 | 17.6 | 13.5 | 12.6 | 12.5 | 12.4 | 12.4 | 12.3 | 12.2 | 12.0 | 11.9 | 11.9 | 11.5 |
| | Score | 1530 | 1418 | 1343 | 1343 | 1333 | 1328 | 1324 | 1313 | 1307 | 767.5 | 761 | 425 | 299 | 299 | 295.5 | 284 | 280 | 272 | 208 | 194 | 193 | 191 | 191 | 190 | 188 | 185.5 | 183 | 183 | 177 |
| | Result No. | | 8 | ٣ | 4 | S | 9 | 7 | œ | o, | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

| hypothetical prote promastiqute surfa | hypothetical prote | mucin - rhesus mac | mucin 5AC (clone J | mucin MUC5B, trach | glucan 1,4-alpha-g | hypothetical prote | mucin, tracheal (A | ascites sialoglyco | zonadhesin - pig | promastigote surfa | mucin 5AC (clone J | I71-7 protein - fr | membrane glycoprot | membrane glycoprot |
|--|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T29634 S20074 | T34369 | 151920 | 853363 | T45025 | 548478 | E86185 | A37232 | A53577 | T34022 | S20075 | 853362 | 862335 | T45462 | T45463 |
| 01 01 | N | ď | N | ~ | - | ~ | 4 | N | N | ~ | N | ~ | ~ | 7 |
| 825 | 1777 | 216 | 279 | 3570 | 1367 | 402 | 294 | 1630 | 2476 | 371 | 477 | 393 | 998 | 867 |
| 11.3 | 7 | -: | 0: | 0 | 0 | 6.0 | 8. | 8. | | 9. | 9.6 | 4-(| 4. | 4. |
| ## | 11 | Ξ | 11 | Ξ | 11 | 10 | 10 | 7 | H | 10 | 7 | 7 | 7 | Ħ |
| 175 | 172.5 | 171.5 | 170.5 | 170 | 169.5 | 168 | 167.5 | 167.5 | 164.5 | 163 | 163 | 160.5 | 160.5 | 160.5 |
| 30 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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| ĕ | K |
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major surface glycoprotein G - human respiratory syncytial virus (strain Long)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: A32703; S12279
R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Matl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A;Reference number: A32703; MUID:87289657; PMID:2441388

A; Accession: A32703

A; Molecule type: mRNA A; Redidues: 1-298 «COND. A; Cross-references: GB:M7212; NID: 9333940; PIDN: AAA47411.1; PID: 9333941 A; Cross-reference. B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A. RNBO J. 9, 4181-4187, 1990 A; Title: Frame shift mutations as a novel mechanism for the generation of neutralizati A; Reference number: \$12279; MUID: 91065351; PMID: 2249671

A; Accession: \$12279
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1.298 < GAR>
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Seywords: glycoprotein; transmembrane protein
B; 41-63, Domain: transmembrane #status predicted < TMN>
P; 41-63, Domain: transmembrane #status predicted < TMN>
P; 41-63, 135, 179, 237, 250, 251, 273, 294, Binding site: carbohydrate (Asn) (covalent) #stat

Gaps ö Length 298; 2; Indels 99.1%; Score 1530; DB 1; 99.0%; Pred. No. 2.3e-92; tive 1; Mismatches 2; Query Match Best Local Similarity 99.04 Matches 295; Conservative

ö

1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60 ò

1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSIAQITLSILAMIISTSLIITAII 60 a

61 FIASANHKVILTTAIIQDATSQIKNTTPTYLLTQDPQLGISFSNLSBITSQTTTILASTTP 120 61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120 à 셤

121 GVKSNLOPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180 ઠે

121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVFCSICSNNP 180 a

181 TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEBPTINTTK 240 181 TCMAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKPTEEPTINTTK 240 ò ద

241 INITITLINNTIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298 ਨੇ

241 TNIITTLITMNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298

RESULT 2

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Gaps

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23; Indels

Length 297;

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1 MSKNKDQRTAKTLERTWDTLNHLLFISSCLYKLNLKSVAQITLSILAMIISTSLIIVAII
                                                                                                    1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
     ; Score 1343; DB 2;
; Pred. No. 3.1e-80;
11; Mismatches 23;
  Query Match
Best Local Similarity 88.6%;
Matches 263; Conservative 1:
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                                                                                                                                                                                                                                                                                           A; Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid protein A; Note: this protein may carry 40-80 separate 0-linked carbohydrate chains distributed a R; Satake, M.; Coligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S. Nucleic Acids Res. 13, 7795-7812, 1985
A; Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure. A; Reference number: A93599; MUID:86067198; PMID:4069997
                                                                                                                                                                                                                                                                            쁑
                       C; Species: human respiratory syncytial virus
C; Species: human respiratory syncytial virus
C; Jozte: 28-May-1996 #sequence revision 28-May-1996 #text_change 24-Sep-1999
C; Accession: A94048; A93599; A04039
R; Wertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.
Byco. Natl. Acad. Sci. US. A. 82, 4075-4079, 1985
A; Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus
A; Reference mumber: A94048; MUID: 85216636; PMID: 3858865
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C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-298 <WER>
A;Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-297 <CAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory
ildren and adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, COSB-references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;38-66/Domain: transmembrane #Ftus predicted <TNM>
F;38-66/Domain: transmembrane #Ftus predicted <TNM>
F;85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (G) protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  attachment protein - human respiratory syncytial virus (strain RSB1734)
NyAlternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKNKDORTAKTLEKTWDTLAHLLFISSGLYKLALKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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91.8%; Score 1418; DB 1; Length 298;
Best Local Similarity 93.3%; Pred. No. 4.2e-85;
Matches 278; Conservative 6; Mismatches 14; Indels
major surface glycoprotein G - human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: JQ1205
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment A;Reference number: JQ1204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: A93599
A, Molecule type: mRNA
A, Residues: 1-298 <SAT>
                                                                                                                                                                                                    A; Accession: A94048
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C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attachment protein - human respiratory syncytial virus (strain RSB6256)
NyAlternate names: G protein
Cispecies: human respiratory syncytial virus
Cispecies: human respiratory syncytial virus
Cibate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
CjAccession: JQ1208 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
CjAccession: JQ1208 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
CjAccession: JQ1208 #sequence long for the attachment (G) protein of subgroup
A; Title: Identification of variable domains of the attachment (G) protein of subgroup
A; Reference number: JQ1204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-297 <CAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
ildren and adults.
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61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP
                                                                                                                                 GVKSNLQPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP
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Pred. No. 3.1e-80;
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87.0%; Score 1343; D
Best Local Similarity 88.5%; Pred. No. 3.1e
Matches 262; Conservative 8; Mismatches
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C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Reywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predi
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: 401207
R;Cans. Matchews, D.A.; Pringle, C.R.
J. Gen. Vivol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Accession: JQ1206
R; Cane, P.A.; Matthews, D.A.; Pringle, C.R.
Gen. Virol. 72, 2091-2095, 1991
A; Title: Identification of variable domains of the attachment (G) protein of subgroup A; Reference number: JQ1204; MUID: 91374005; PMID:1895054
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                 61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFSNLSETTSQPATTPALTTP 120
                                                                                                                                           TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPOTTKPKEVPTTKPTEEPTINTTK 240
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Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
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N;Alternate names: G protein
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87.8%; Pred. No. 5.3e-79;
tive 7; Mismatches 29;
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Best Local Similarity
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A; Residues: 1-297 <CAN>
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A; Molecule type: mRNA
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N.Alternate names: G protein
C,Species: human sespiratory syncytial virus
C,Species: human sespiratory syncytial virus
C,Species: human sespiratory syncytial virus
C,Species: human sespiratory syncytial virus
C,Accession: J01209

R,Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. virol. 72, 2091-2096, 1991
A,Title: Identification of variable domains of the attachment (G) protein of subgroup A,ATitle: Identification of variable domains of the attachment (G) protein of subgroup A,ATITLE: Identification of variable domains of the attachment (G) protein of subgroup A,ANCecession: J01209
A,Molecule type: mRNA
A,Residues: 1-297 cCAN>
C,Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il cr children and adults.
C;Comment: respiratory syncytial virus major surface glycoprotein G
C;Reywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
G protein - Human respiratory syncytial virus
C,Species: Human respiratory syncytial virus
C,Species: Human respiratory syncytial virus
C,Species: Human respiratory syncytial virus
C,Accession: JC5600
C,Accession: JC5600
C,Accession: JC5600
A,Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain is
A,Reference number: JC5600
A,Reference number: JC5600
A,Respiratory syncytial virus strain is
A,Respiratory syncytial virus major surface glycoprotein G
C,Superfamily: respiratory syncytial predicted <INT>
F;37-266/Domain: intracellular #status predicted <INT>
F;37-286/Domain: extracellular #status predicted <INT>
F;67-298/Domain: Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure Figure 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 86.3%; Score 1333; DB 2; Length 298; al Similarity 87.9%; Pred. No. 1.4e-79; 262; Congervative .10; Mismatches 26; Indels (
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Best Local S
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MGNZ18
                                                                                              RESULT 10
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                        22.4
                                                                    C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
P;85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
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              A,Note: the authors translated the codon ACC for residue 4 as Asn and AGC for residue C,Comment: Respiratory syncytial virus commonly causes severe lower respiratory tractildren and adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus
31-Mar-1992 #text_change 16-Feb-1997
                                                                                                                                                                                                                                      121 GVKLTLQSTTVRIKNTTTTQAQPNKSTTKQRQNKPPSKPNNDFHFEVPNFVPCSICSNNP
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                                                                                                                                                                                                                                                                                        FIASANHKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTP
                                                                                                                                                                                                                                                                                                                          61 FIASANNKVTLTTAIIQDATSQIKNTTPTYLTQNPQLGISFFNLSGTTSQTTAILALTTP
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                                                                                                                                           85.0%; Score 1313; DB 2; Length 298; larity 86.9%; Pred. No. 2.7e-78; Conservative 11; Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.7%; Score 1307; DB 2; Length 297;
86.5%; Pred. No. 6.7e-78;
ive 12; Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_chang
C;Accession: JQ1204
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment
A;Reference number: JQ1204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 attachment protein - human respiratory syncytial virus N;Alternate names: G protein
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                                                                                                                                                          Similarity
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A, Molecule type: mRNA
A, Residues: 1-297 < CAN>
A;Residues: 1-298 <CAN>
                                                                                                                                                             Local Simi
hes 259;
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Best Local S:
Matches 259
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Best Local S:
Matches 257,
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major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N;Alternate names: attachment glycoprotein G
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A37077
R;Sullender, W.M.; Anderson, K.; Wertz, G.W.
A;Iulles: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of gous subgroup virus challenge.
A;Reference number: A37077; MUID:90357765; PMID:1697126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A37077
MyOlecule type: mRNA
A;Residues: 1-292 <SVII.>
A;Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKHKNQRTASTLEKTWDTLAHLIVISSCLYRLNLKSIAQIALSVLAMIISTSLIJAAII
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                     241 TNIITTPLTSNTARNPELTSQMETFHSTSSEGNPSPSQVSITSEYPPQPSSPPNTPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: respiratory syncytial virus major surface glycoprotein C;Keywords: glycoprotein; transmembrane protein cransmembrane F;45-63/Domain: transmembrane #status predicted <TMN> F;45-63/Domain: transmembrane #status predicted <TMN> F;81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #statu
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es 94; Indels
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49.7%; Score 767.5;
Best Local Similarity 55.3%; Pred. No. 6.4e
Matches 162; Conservative 34; Mismatches
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major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: B32703
R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A;Reference number: A32703; MUID:87289657; PMID:2441388 A,Accession: B32703 A,Molecule type: mRNA A,Molecule type: mRNA A,Fesdidues: 1-222 <JOH> A,Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943 C;Superfamily: respiratory syncytial virus major surface glycoprotein G C;Keywords: glycoprotein; transmembrane protein F;41-63/Domain: transmembrane #status predicted <TMN> F;81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

ä

49.3%; Score 761; DB 1; Length 292

| Best Local Similarity 54.9%; Pred. No. 1.7e-42; Matches 158; Conservative 35; Mismatches 93; Indels 2; Gaps 2; | F;60-250/Domain: F;78,156,226,241 | , 2 e |
|---|--|--|
| Qy 1 MSKNKDQRTAKTLEKTWDTLAHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60 | Query Match Best Local Sim Matches 91; | Simila |
| OY 61 FIASANHKVTLTTAIIQDATSQIKNTTPTVLTQDPQLGISFSNLSBITSQTTTILASTTP 120 | 9y 11 K | KTLE |
| OY 121 GVKSNLQPTTVKTKNTTTOTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180 | Qy 71 L7 Db 64 P7 | LTTA : PTSK |
| QY 181 TCWAICKRIPNKKPGKKTTTKPTKKTF-KKDLKPQTTKPKEVPTTKPTEBPTINTT 239 | Oy 131 W | VKTKO |
| Oy 240 KTNITTLLINNTTGNPKLISQMETPHSISSEGNLSPSQVSTTSEHPS 287 : : : : | Oy 179 Ni | NPTC - NLAC |
| | QY 239 TI | TKTN |
| RESULT 12 NHNZ NHNZ NHOLOCOEPSID protein (version 2) - human respiratory syncytial virus C;Species: human respiratory syncytial virus C;Species: human respiratory syncytial virus C;Accession: A04026 R;Elango, N.; Venkatesan, S. Nucleic Acids Res. 11, 5941-5951, 1983 Nucleic Acids Res. 11, 5941-5951, 1983 A;Title: Amino acid sequence of respiratory syncytial virus capsid protein. | RESULT 14 MGNZBR major surface glyco N;Alternate names: C;Species: bovine | glyca ines: |
| A. Accession: A04026 A. Accession: A04026 A. Molecule type: mRNA A. Residues: 1-467 < KLA> C. Genetics: 6B:X00001; NID:g61215; PIDN:CAA24906.1; PID:g61216 A. Genetics: 0.00000000000000000000000000000000000 | C,Accession: A3640 R;Lerch, R.A.; And J, Virol. 64, 5559 A;Title: Nucleotid y syncytial virus: A,Reference number A,Reference number | 640 drid drid drid drid 640 |
| Query Match Query Match Best Local Similarity 90.2%; Score 425; DB 1; Length 467; Matches 83; Conservative 3; Mismatches 6; Indels 0; Gaps 0; | A, Residues: 1-22 A, Cross-referency G, Genetics: A, Gene: G | . 537 Cee |
| Qy 207 TEKTTKKOLKPQTTKPKEVPTTKPTEBPTINTTKINITTLLINNTTGNPKLJSQMBTFH 266 | C;Superramily: 3 C;Keywords: glyor; F;45-62/Domain: F;3,85,127,149; | 33 t G |
| Oy 267 STSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298 | Query Match Best Local Simil Matches 92; C | lif. |
| RESULT 13 PQ0768 Glycoprotein G - bovine respiratory syncytial virus (isolate FS-1) (fragment) C,Species: bovine respiratory syncytial virus C,Date: 14-Jul-1994 #sequence revision 14-Jul-1994 #text change 07-May-1999 | 2y 1 Mi Db 1 Mi 2y 61 F | MSKN : MSNH FIAS |
| C.Accession: PQ0768 RMallipeddi, S.K.; Samal, S.K. J. Gen. Virol. 74, 2001-2004, 1993 A.Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial v A.Reference number: JQ2284; MUID:93389461; PMID:8376974 | Db 61 Y. Oy 121 G | YISV |
| A;Molecule type: mRNA A;Residues: 1-250 <mal> C;Cuperfamily: respiratory syncytial virus major surface glycoprotein G C;Keywords: glycoprotein; transmembrane protein F;1-31/Domain: intracellular #status predicted <ivm></ivm></mal> | Qy 169 Ni Db 169 Pi Qy 229 Ki | NFVP : PYVP KPTE : |
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de sequence analysis and expression from recombinant vectors demonst;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ## sepiratory syncytial virus major surface glycoprotein G
**protein, transmembrane protein
**ransmembrane # status predicted (TMN)
**3,251/Binding site: carbohydrate (Asn) (covalent) # status predicted
extracellular #status predicted <BXT>
244/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roprotein G - bovine respiratory syncytial virus (strain 391-2) is atteachment glycoprotein G is respiratory syncytial virus (srepiratory syncytial virus 92 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNITITOTOPSK-----PTIKO-----RONKPPNKPNNDFHFEVFNFVPCSICSN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGHSTDETÓSRKIKSQSTLPTTRKPPINPSESNPPENHQDHNNSQTLPYVPCSTCEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NITITLLINNTIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGNAKAKPTSKPTIQQTQQPQNHTSPFFTEHNY------KSTHTSIQSTTL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNLQPITVKTKNTTTTQTQPSK---PTTKQRQNKPPNKPNNDF-------HFEVF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTT 228
                                                                                                                                                                                                                                                                                                                                                                           ALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTHELKPRILKRAMKASKYFIVGLSCLYKFNLKSLVQTALSTLAMITLITSLVITAII 60
                                                                                                                                                                                                                                      EKTWDTLNHLLFISSGLYKUNKSVAQITLSILAMIISTSLIITAIIFIASANHKVT 70
                                                                                                                                                                                                                                                                             NKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60
                                                                                         19.4%; Score 299; DB 2; Length 250;
larity 30.3%; Pred. No. 1.3e-12;
Conservative 35; Mismatches 104; Indels 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.4%; Score 299; DB 1; Length 257;
.larity 31.6%; Pred. No. 1.3e-12;
Conservative 33; Mismatches 120; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :s: GB:M58307; NID:g210830; PIDN:AAA42810.1; PID:g210831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r: A36408; MUID:91012801; PMID:2214024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nderson, K.; Wertz, G.W. 19-5569, 1990
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Jugocoptein G - bovine respiratory syncytial virus (isolate A51908)
C;Species: bovine respiratory syncytial virus
C;Species: 14-011-1994 #sequence_revision 14-011-1994 #text_change 07-May-1999
C;Accession: J02284
R;Mallipeddi, S.K.; Samal, S.K.
J. Gen. Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial vA;Reference number: J02284; MUID: 93389461; PMID: 8376974
A;Reference number: J02284; MUID: 93389461; PMID: 8376974
A;Reference number: J02284; MUID: 93389461; PMID: 8376974
A;Reference number: J02284; MUID: 93899461; PMID: 8376974
A;Reference number: J02284; MUID: 93899461; PMID: 8376974
C;Superimental source: isolate A51908
C;Superimental source: isolate A51908
C;Superimental source: isolate A51908
C;Superimental source: scalar status predicted <CTMA:
F;39-66/Domain: intransmembrane #status predicted <CTMA:
F;39-66/Domain: extracellular #status predicted <CTMA:
F;27-263/Domain: extracellular #status predicted <CTMA:
F;127,163,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FIASANHKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GVK-----SNLOPITVKIKNT-TITQTQPSKPITKQRQNKPNKPNKPNNDFHFEVFNFVPCS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 GTTYGHPINRTÖNRKIKSGSTPLATRKLPINPL----ESNPPENHQDHNNSQTLPHVPCS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 ICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLKPQTTKP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 TCEGNPACSPLCQIGLERAPSRAPTITLKKAPKPKTTTYHRTSPEAKLQTKKN 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
19.1%; Score 295.5; DB 2; Length 263;
Best Local Similarity 31.7%; Pred. No. 2.3e-12;
Matches 86; Conservative 35; Mismatches 123; Indels 27; Gaps
213 KPTK--TTIHHRTSPETKLQPKNNTATP----QQGILSSTEHHTNQSTTQI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 KEVPITKPIEEPIINTIKINITILLINNIT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATPQQGILSSP---EHQTNQSTTQISQHTS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: October 29, 2003, 17:41:49
Job time: 31.6755 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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October 29, 2003, 17:41:00 ; Search time 52.2906 Seconds (without alignments) 975.349 Million cell updates/sec OM protein - protein search, using sw model Run on:

1 MSKNYDQRTAKTLEKTWDTL......vsttsehpsqpssppnttrq 298 US-09-462-816-2 1544 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 642050 segs, 171146064 residues Searched:

642050

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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|---------------|-------|----------------|--------------------------|----|---------------------|-------------------|
| Result No. | Score | Query Match | Query Match Length DB | DB | ΩI | Description |
| | 193 | 12.5 | <u> </u> | 6 | US-09-922-217-1068 | Sequence 1068, Ap |
| 7 | 193 | 12.5 | - | 10 | US-09-833-263-1068 | Sequence 1068, Ap |
| ٣ | 193 | 12.5 | 5179 | 14 | US-10-025-380-1068 | Sequence 1068, Ap |
| 4 | 177.5 | 11.5 | | 12 | US-10-029-386-32198 | Sequence 32198, A |
| ß | 169.5 | 11.0 | | 10 | US-09-801-368-108 | Sequence 108, App |
| Y | 169 | 10.9 | | 12 | US-10-351-641-871 | Sequence 871, App |
| 7 | 162.5 | 10.5 | 288 | σ | US-09-216-393-341 | Sequence 341, App |
| æ | 162.5 | 10.5 | | Q | US-09-216-393-344 | Sequence 344, App |
| o, | 162.5 | 10.5 | | 12 | US-10-321-856-341 | Sequence 341, App |
| 10 | 162.5 | 10.5 | | 12 | US-10-321-856-344 | Sequence 344, App |
| 11 | 162 | 10.5 | | 14 | US-10-124-557-14 | Sequence 14, Appl |
| 12 | 162 | 10.5 | | 14 | US-10-124-557-84 | Sequence 84, Appl |
| 13 | 162 | 10.5 | | 14 | US-10-124-557-74 | Sequence 74, Appl |
| 14 | 162 | 10.5 | | 14 | US-10-124-557-58 | Sequence 58, Appl |
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| sequence 44, Appl Sequence 42, Appl Sequence 50, Appl Sequence 60, Appl Sequence 60, Appl Sequence 48, Appl Sequence 52, Appl Sequence 52, Appl Sequence 62, Appl Sequence 20, Appl Sequence 3, Appli Sequence 110, Appl Sequence 110, Appl Sequence 110, Appl Sequence 111, Appl Sequence 21, Appl Sequence | 21222222 |
|---|---|
| 10-1224 10-122 | 10-176-847-5 10-137-293-1 10-137-870-2 110-140-018-2 110-140-274-2 110-140-471-2 |
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| 11327 11317 | 22 82 2 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |
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| 162 162 162 162 162 162 162 162 163 163 163 163 163 163 163 163 163 163 | 0.000000000000000000000000000000000000 |
| 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 8001244444 |

ALIGNMENTS

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71 LITALIQDA--ISQIXNITP----IYLIQDPQLGISFSNLSEIT--SQTTILLASTIPG 121
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Best Local Similarity 30.6%; Pred. No. 2.3e-06;
Matches 77; Conservative 23; Mismatches 114; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Clapper, Jonathan D. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE FILE REFRENCE: 210121.471C13 CURRENT APPLICATION WUMBER: US/09/922,217 CURRENT FILING DATE: 2001-08-03 NUMBER: OF SEQ ID NOS: 1124 SOFTWARE: PASSES OF Windows Version 4.0 SEQ ID NO 1068 LENGTH: 5179
                                                  Sequence 1068, Application US/09922217
Patent No. US20020076414A1
                                                                                                                              APPLICANT: Xu, Jiangchun
APPLICANT: Sucrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Ming, John A.
APPLICANT: Mang, Tongtong
APPLICANT: Sidth, Garole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-922-217-1068
                                                                                                          GENERAL INFORMATION:
                             JS-09-922-217-1068
RESULT 1
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Sequence 32198, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: REAL DAVID R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOUTHARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 32198
LENGTH: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1676 PPITTPSS-TITTPSSPTTTP--SSPITTTP--SSTTTPSSTTTTPS 1731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 LTTAIIQDA--TSQIKNTTP-----TYLTQDPQLGISFSNLSBIT--SQTTTILASTTPG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ----VKSNLQPTTVKTKNTTTT------QTQPSKPTTKQRQNKPPNKPNNDFH 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 VPTTKPTEEPTINTTKTNITTLLTNNTTGNPKLTSOMETFHSTSSEGNLSPSOVSTTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.5%; Score 193; DB 14; Length 5179; Best Local Similarity 30.6%; Pred. No. 2.3e-06; Matches 77; Conservative 23; Mismatches 114; Indels 38;
                                                                                                                                                                                       APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1129
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
        Madeleine Joy
                                                                                  Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
Wang, Aijun
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1732 SPTTTPSPPTT 1743
Meagher, Madelei
Stolk, John A.
Wang, Tongtong
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US-10-029-386-32198
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APPLICANT:
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                                                  1564 PPPTTTTPPPPTTTPSPPTTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTT 1623
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                                                                                                           165 FEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKB 224
                                                                                                                                                                                                                    225 VPITKPIEEPIINTIKTNITILLINNTIGNPKLISQMETFHSISSEGNLSPSQVSTISE 284
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     -----QTQPSKPTTKQRQNKPPNKPNNDFH 164
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APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: State of Liabper, Jonathan D.
APPLICANT: State of Liabper, John A.
TITLE OF INVENTION: COMPOUNDS POR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471212
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1068
LENGTH: 5179
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12.5%; Score 193; DB 10; Length 5179;
Best Local Similarity 30.6%; Pred. No. 2.3e-06;
Matches 77; Conservative 23; Mismatches 114; Indels 38; Gaps
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US-10-025-380-1068
; Sequence 1068, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1068, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
  ----VKSNLQPTTVKTKNTTTT
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COGGANISM: Homo sapiens
US-09-833-263-1068
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  122
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140 QTQPSKFTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTT 199
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Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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ORGANISM: Toxoplasma gondii
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SEQ ID NO 341
LENGTH: 288
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US-10-351-641-871
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FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 KNTIPIYLIQDPQLGISFSNLSEITSQTTTILASTIPGV--KSNLQPTTVKTKTKTTT--T 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 VTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQP 128
                                                                                                                                                                                                                                                                                                                                                            129 TTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKR 188
                                                                                                                                                                                                                                                                                                                                                                                                    ----TITITSTITIT 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAIIFIASANHK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 -TTTLLTNNTTGNPKLTSQMBTFHSTSSBGNLSPSQVSTTSEHPSQPSSPP 293
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                                                                                                                                                              35;
                                                                                                                    11.5%; Score 177.5; DB 12; Length 800; 23.7%; Pred. No. 3.9e-06; tive 39; Mismatches 148; Indels 35;
  OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR PILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-0
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 108
LENGTH: 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
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ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                        441 TTITITSTTTTTTTTT---
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
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                                                                                                                                         Best Local Similarity 23.7% Matches 69; Conservative
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Silva, Jeff
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Summers, Eric
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Milne, Todd
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                                                                 ; OTHER INFURMALLY
US-10-029-386-32198
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APPLICANT:
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Patent No. US2010014447A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TOXOPLASMA GONDI! PROTEINS, NUCLEIC ACID MOLECULES, AND TITLE OF INVENTION: TX-1-C2
TITLE OF INVENTION: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
BARLIER APPLICATION NUMBER: 08/994,825
NUMBER OF SEQ ID NOS: 364
269 KEKPIPPITISCIKEKPIPPHHD-----ITPCI------KKKITISKICIKKI 310
                                                                                                                                                                                                                                                               311 TTPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAP 370
                                                                                                                                                                                        200 TKPTKKPTFKTTKKDLKP-----QTTKPKBVPTTKPTEB-----PTINTTKTNITTL 247
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APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, M.
APPLICANT: Lambert, D.
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10.9%; Score 169; DB 12;
Best Local Similarity 94.4%; Pred. No. 3.5e-07;
Matches 34; Conservative 1; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PLICATION NUMBER: 09/315,304
PRIOR PLICATION NUMBER: 09/315,304
PRIOR PLICATION NUMBER: 09/082,279
PRIOR PLILNG DATE: 1998-05-20
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-216-393-341
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RESULT 10
US-10-321-856-344
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LENGTH: 288
                                                                                                                                                                                                                                                                                   TYPE: PRT
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Patent No. US20010014447A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASNA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND TITLE OF INVENTION: USES THEREOF
FILE REPRENCE: TX.1-C2
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER PILING DATE: 1999-12-19
SEARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                               76 AALSTDAIDRVSQFDLVSLLDVIRRAAQAKFDLLGRLIITDIASGIGBGAMALMGERAAFI 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KNTIPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                                                                                         -----KNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKN 135
                                                                                                                                                                                                                                                                                196 KKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTTLLTNNTTGN 255
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                                                                                                                                                                                                                                                                                                               Gaps
                                     95;
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10.5%; Score 162.5; DB 9; Length 288; 23.1%; Pred. No. 1.8e-05; Live 22; Mismatches 99; Indels 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 23.1%; Pred. No. 1.8e-05;
Matches 65; Conservative 22; Mismatches 99; Indels 95
                                                                      39 AQITLSILAMIISTSLIITAIIFIASANHKVTLTTAIIQDATSQI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Toxoplasma gondii
US-09-216-393-344
                  Best Local Similarity 23.19
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-216-393-344
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LENGTH: 288
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 Query Match
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RESULT

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APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
FILE REFERENCE: TX-1-C2-1
CURRENT APPLICATION NUMBER: US/10/321,856
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR PILING DATE: 1999-12-18
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 341
LENGTH: 288
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TITIE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER PILE REPERENCE: TX-1-C2-1
CURRENT APPLICATION NUMBER: US/10/321,856
CURRENT APPLICATION NUMBER: 02/216,393
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 -----KNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local Similarity 23.1%; Pred. No. 1.8e-05;
Matches 65; Conservative 22; Mismatches 99; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 288;
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; Sequence 341, Application US/10321856; Publication No. US20030194393A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Toxoplasma gondii
US-10-321-856-341
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Best Local Similarity
Matches 65; Conserv
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136 TTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPG 195
                                                                                                                                                                                                                                                         196 KKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTTLLTNNTTGN 255
                                                                                                                                                                                                                                                                                                     84 -----KNTTPTYLTQDPQLGISFSNLSEITSQTTTTILASTTPGVKSNLQPTTVKTKN 135
                                                                                                                    RESULT 11
US-10-124-557-14

Sequence 14, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clastk, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION APPL.

PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-APN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DUN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GI 5190 TELLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-124-557-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 941 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                           132 K-----TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 NPTCWAICKRIPN-----KKPGKKTTTKP-------TKRPTFKTTK 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 KDL----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLITNNTTGNPKLTS 260
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                                                                                                        Gaps
                                                                                                   78;
10.5%; Score 162; DB 14; Length 941; 24.6%; Pred. No. 9e-05; Live 26; Mismatches 104; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 TTKSAPTTPKE----PSPTTTKEPAPTTPKEPAPTT 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 84, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
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STATE: Massachusetts
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                                                                                                   Conservative
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02140
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                                                                                                   Matches
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TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
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US-10-124-557-58
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                                                                                                                                                     Gaps
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                                                                                                       10.5%; Score 162; DB 14; Length 1022; 24.6%; Pred. No. 0.0001; tive 26; Mismatches 104; Indels 78
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Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney W.
Genneth
TITLE OF INVENTION: Hegakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                   254 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP
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STREET: 87 CambridgePark Drive
CITY: Cambridge
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
APPLICATION NUMBER: US 07/457,196
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
      MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 84:

US-10-124-557-84
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COMPUTER READABLE FORM:
                                                                                          Query Match
Best Local Similarity 24.6%;
TOPOLOGY: linear
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US-10-124-557-74
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                                                                                                                                                                                  Length 1038;
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Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                       Query Match
10.5%; Score 162; DB 14; Length 1
Best Local Similarity 24.6%; Pred. No. 0.0001;
Matches 68; Conservative 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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STREET: 87 CambridgePark Drive
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CLASSIPICATION: -OUKNOWN.>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/124,557
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      74:
                            ; TOPOLOGY: Inhear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
LENGTH: 1038 amino acids
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COMPUTER READABLE FORM:
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Search completed: October 29, 2003, 17:54:26 Job time : 54.2906 secs
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                                                                                                                                                                                                                                                                                                                          10.5%; Score 162; DB 14; Length 1049; 24.6%; Pred. No. 0.0001; tive 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-Apr-2002
CLASSIFCATION: -4Dr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, Stephen C.
Jacobs, Renneth
Hewick, Rodney M.
Gesner, Thomas G.
INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
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NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERESTICS:
LENGTH: 1049 amino acids
TYPE: amino acids
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FILING DATE: 18-UAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-124-557-58
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ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
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STATE: Massachusetts
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                       68; Conservative
                                                                                                                                                                                                                                                                                                                                                   Similarity
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US-10-124-557-104
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Matches
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131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 APTITKSAPITPKEPAPITPKKPAPITPKEPAPITPKEPTPKEPAPITKEPAPITKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 KDL-----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLTNNTTGNPKLTS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 TTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV
                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                                                                                                                 Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                              26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 TIKSAPITPKE---PSPITIKEPAPIT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 296
                                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 162; DB 14;
24.6%; Pred. No. 0.00012;
APPLICATION NUMBER: US 07/457,196
             FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                 5190
                                                                                                                                                                                                                                                          TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 NPTCWAICKRIPN----KKPGKKTTTKP
                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CSert. Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 29, 2003, 17:36:05; Search time 16.3057 Seconds (without alignments) 773.267 Million cell updates/sec

US-09-462-816-2 Perfect score:

1 MSKNKDQRTAKTLEKTWDTL......VSTTSEHPSQPSSPPNTTRQ 298 Sequence:

Scoring table:

328717 seqs, 42310858 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2_6/ptodata/2/jaa/5A COMB.pep:*
2: /cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | ₩ | | | | |
|---------------|-------|----------------|--------|----|--------------------|-------------------|
| Result No. | Score | Query Match | Length | DB | ΔI | Description |
| 1 | 1544 | 100.0 | 298 | ~ | US-08-467-963C-8 | Sequence 8, Appli |
| (3 | 1544 | 100.0 | 298 | ~ | US-08-838-189D-8 | œ |
| ო | 1544 | 100.0 | 298 | m | US-08-852-344D-8 | Sequence 8, Appli |
| 4 | 1544 | 100.0 | 298 | m | US-08-344-639E-8 | æ` |
| 5 | 1544 | 100.0 | 298 | ო | US-08-467-969A-8 | w |
| 9 | 1544 | 100.0 | 298 | m | US-08-467-961A-8 | ω |
| 7 | 1544 | 100.0 | 298 | m | US-08-001-554A-8 | Sequence 8, Appli |
| 80 | 901 | 58.4 | | 9 | 5194595-19 | |
| σ | 295.5 | 19.1 | | ഗ | PCT-US91-08177-13 | Sequence 13, Appl |
| 10 | 222 | 14.4 | 37 | ო | US-08-793-792-12 | 12, |
| 11 | 193 | 12.5 | 32 | m | US-08-793-792-8 | 8 |
| 12 | 188 | 12.2 | 216 | m | US-08-928-361B-8 | œ |
| 13 | 188 | 12,2 | 216 | 4 | US-09-588-995A-8 | œ |
| 14 | 188 | 12.2 | | m | 1 | 'n |
| 15 | 188 | 12.2 | 1837 | 4 | US-09-588-995A-5 | Sequence 5, Appli |
| 16 | 187.5 | 12.1 | | ٣ | US-08-700-651-5 | 'n |
| 17 | 187.5 | 12.1 | - | ო | US-08-928-361B-6 | Sequence 6, Appli |
| 18 | 187.5 | 12.1 | 1721 | 4 | US-09-588-995A-6 | ģ |
| 19 | 183.5 | 11.9 | 7 | ო | US-08-928-361B-27 | 27 |
| 20 | 174 | 11.3 | | ო | US-08-793-792-4 | 4 |
| 21 | 173.5 | 11.2 | | m | US-08-700-651-15 | 15, |
| 22 | 173.5 | 11.2 | | m | US-08-928-361B-20 | 20, |
| 23 | 173.5 | 11.2 | N | 4 | US-09-588-995A-20 | |
| 24 | 169 | 10.9 | 36 | m | US-09-082-279B-871 | 871 |
| 25 | 169 | 10.9 | | 4 | US-09-315-304B-871 | 87 |
| 26 | 169 | 10.9 | | 4 | US-09-834-784-871 | 87 |
| 27 | 164.5 | 10.7 | 2476 | N | US-08-276-967-2 | Sequence 2, Appli |

| Sequence 341, App | Seguence 344, App | | Sequence 84, Appl | | | | | Sequence 42, Appl | | Sequence 50, Appl | Sequence 46, Appl | Sequence 60, Appl | Sequence 48, Appl | Sequence 40, Appl | Sequence 52, Appl | Sequence 2, Appli | Seguence 62, Appl |
|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| US-09-216-393B-341 | US-09-216-393B-344 | US-07-757-022B-14 | US-07-757-022B-84 | US-07-757-022B-74 | US-07-757-022B-58 | US-07-757-022B-104 | US-07-757-022B-44 | US-07-757-022B-42 | US-07-757-022B-142 | US-07-757-022B-50 | US-07-757-022B-46 | US-07-757-022B-60 | US-07-757-022B-48 | US-07-757-022B-40 | US-07-757-022B-52 | US-07-757-022B-2 | US-07-757-022B-62 |
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| 288 | 288 | 941 | 1022 | 1038 | 1049 | 1140 | 1270 | 1311 | 1313 | 1314 | 1320 | 1320 | 1354 | 1361 | 1363 | 1404 | 1404 |
| 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 | 10.5 |
| 162.5 | 162.5 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 |
| 28 | 53 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

```
Sequence 8, Application US/08467963C
Patent No. 5968776
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: EMASYSHYN, Mary E
TITLE OF INVENTION: CHILTIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINPLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC. COMPATIBLE
OPERATING SYSTEM: PC. DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1038-474 MIS:jb
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSES: Sim & Meburney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION NUMBER: US/08/191/5050
REIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTENISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-467-963C-8
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RESULT 1
US-08-467-963C-8
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Sequence 8, Application US/08852344D Patent No. 6017539
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                        Matches 298; Conservative
                                                                    Query Match
Best Local Similarity
JS-08-838-189D-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-852-344D-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08838189D
Parent No. 5998169
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: WIN-Pan
APPLICANT: BWASYSHYN, Mary E
TITLE OF INVENTION: MULTIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENCA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                 61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
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                                                                                                                                                                              1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
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                              100.0%; Score 1544; DB 2; Length 298; 100.0%; Pred. No. 2.1e-132;
                                                                                                         Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION NUMBER: GB 9200117.1
PLING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-687 MIS:jb
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID 05
INFORMATION SEQ ID 05
INFORMATION SEQ ID 06
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                                                                                                  0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                              Ouery Match
Best Local Similarity 100.
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
COUNTRY: Canada
ZIP: MSG IRT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                                                                                                                                 121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVPUFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TCWALCKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
                                                                                                                                                                                                                                                                                                                                                   121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TCWALCKRIPNKKPGKKTTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
                                                                                                                                                                            09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TNITTILLTUNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPDNTTRQ 298
                                                                                                                    1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                      1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: KLEIN, Michel H
APPLICANT: EWASYSHYN, Mary E
TITLE OF INVENTION: CHIMBRIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                              ö
  Length 298;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: COCONTO

CITY: COLONICO

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639

FILING DATE: 07-MAY-1997

CLASSIFICATION NUMBER: US 08/344,639

FILING DATE: 14-NOV-1994

PRIOR APPLICATION NUMBER: GB 9200117.1

PRILING DATE: 06-JAN-1992

ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,973

RERERENCE/DOCKET NUMBER: 24,973

RELEPHONE: (416) 595-1163

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE (TRRACTERISTICS:
TEMBERAL 298 amino acids
100.0%; Score 1544; DB 2;
100.0%; Pred. No. 2.1e-132;
tive 0; Mismatches 0;
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STREET: 6th Floor, 330 University Avenue
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SEQUENCE CHARACTERISTICS
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US-08-344-639E-8
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                                                                                                                                                                                                                                                                                                                                                                                                                     121 GVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
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                                                                                                                                                                                                          1 MSKNKDQRTAKTLEKTWDTLAHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                         1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                Gaps
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                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-132;
Matches 298; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: ELUGY LALES
COMPUTER: IEM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44,639E
FILING DATE: 14-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-391 MIS
TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 595-1163
TELEX: 065-24667 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08344639E
Patent No. 6033668
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STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
j TOPOLOGY: linear
US-08-852-344D-8
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US-08-344-639E-8
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61 FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKNKDQRTAKTLEKTWDTLANHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TNITITILINNTTGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298
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COUNTER: CREATED
COUNTER: CREATED
COUNTER: CREATED
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN BATA:
APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/01,554
FILING DATE: 06-JAN-1993
CLASSIFICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION NUMBER: SE 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: RE 9200117.1
FILING DATE: 06-JAN-1992
ATFORNEY/AGENT INPORMATION:
NAME: STEWARY/AGENT INPORMATION:
NAME: STEWARY/AGENT INPORMATION:
TELESTRATION NUMBER: 1038-475 MIS:bh
TELESTROCH/MUNDER: 1038-475 MIS:bh
TELESTROCH/MUNDER: 1055-1155
                                                                                                                                                                        Query Match
100.0%; Score 1544; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.1e-132;
Matches 298; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08467969A

Patent No. 6168786
GENERAL INFORMATION:
APPLICANT: Bu, Run-Pan
APPLICANT: Ewasyshyn, Mary E
ITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
  298 amino acids
                                                      single
LENGTH: 298 amin
TYPE: amino acid
STRANDEDNESS: si
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US-08-467-961A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FIASANHKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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Best Local Similarity 100.0%; Pred. No. 2.1e-132;
Matches 298; Conservative 0; Mismatches 0; Indels 0
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ZIT: Ontario
COUNTRY: Canada
ZIT: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION ATA:
ADDITION NUMBER: US 08/001,554
FILING BATE: 06-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
ADDITION ADDITION DATA:
ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITION ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIONAL ADDITIO
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| Sequence 8, Application US/08467961A
| Sequence 8, Application US/08467961A
| Patent No. 6171783
| GENERAL INFORMATION:
| APPLICANT: Easts Name Pan
| APPLICANT: Easts Name Pan
| APPLICANT: Easts Name Pan
| APPLICANT: Easts Name Pan
| TITLE OF INVENTION:
| UNMER OF SEQUENCES: 21
| CORRESSONDENCE ADDRESS:
| ADDRESSES: Sim & McBurney
| STREET: 330 University Avenue, 6TH Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
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REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-467-969A-8
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TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                       LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
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61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKINLKSVAQITLSILAMIISTSLIITAII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
CONTRY: Canada
ZIP: MAGI IR/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Propsy disk
COMPUTER: Propsy disk
COMPUTER: Propsy disk
COMPUTER: PR PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
CURSSIFICATION: APPLICATION: APPLICATION APPLICATION APPLICATION APPLICATION: APPLICATION APPLICATION APPLICATION APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: APPLIC
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Patent No. 6225091
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Edwaryshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: 21
CORRESPONDENCES: 21
CORRESPONDENCES: 31
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INPORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFONE (416) 595-1155
TELEFAX: (416) 595-1163
TELEFAX: 065-24567 SIMBAS
                                TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1157
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
TENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 298; Conservative
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Best Local Similarity
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 QLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 QLGISPSNPSEITSQITTILASTTPGVKSTLQSTTVKTKNTTTTQTQPSKPTTKQRQNKP 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 PNKPNNDFHFEVFNFVPCSICSNNPTCWAJCKRIPNKKPGKKTTTKPTFKTTKKDL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 KPQTTKPKEVPTTKPTEEPTINTTKTNITTLLITNNTTGNPKLITSQMETFHSTSSEGNLS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 KPQTTKSKEVPTTKPTEEPTINTTKTNIITTLLISNTTGNPELTSQMETFHSTSSEGNPS 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSBITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                        61 FIASANHKVILTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSBITSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                  1 MSKNKDORTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII 60
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                                                                                                                                                                                  Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WATHEN, MICHAEL W.
TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
JIMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                Similarity 100.0%; Score 1544; DB 3; Similarity 100.0%; Pred. No. 2.1e-132; 98; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNCYTLAL VIRUS

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/07/543,780

FILING DATE: 31-0CT-1988

PRIOR APPLICATION NUMBER: 137,387

FILING DATE: 23-DEC-1988
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                        MOLECULE TYPE:
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                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                              Matches 298;
                                                                                                                                            US-08-001-554A-8
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                                                                                                                                                                                     Query Match
Best Local 8
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5194595-19
;Patent No.
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61 PIASANHKVTLITALIQDAISQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GTTYGHPINRTÖNRKIKSQSTPLATRKLPINPL----ESNPPENHQDHNNSQTLPHVPCS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ICSNNPTCWAIC----KRIPN-----KKPGKKTTTKPTKKPTFKTTKKDLKPQTTKP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 TČEGNPAČSPLČQIGLERAPSRAPTITLKKAPKPKŤTKKPTKTTIYHRTSPEAKLÇTKKN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSNHTHHPKFKTLKRAMKASKYFIVGLSCLYKFNLKSLVQTALTSLAMITLTSLVITALI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Gaps
                                                               APPLICANT: Samal, Siba K
TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.1%; Score 295.5; DB 5; Length 263; 31.7%; Pred. No. 4.1e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: INVENTION: Antigenic peptides derived from the
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08177
FILING DATE: 19911104
CLASSIPICATION: 435
PRIOR APPLICATION NUMBER: US 07/608,937
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 TATPQQGILSSP---EHQTNQSTTQISQHTS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 KEVPTTKPTEEPTINTTKTNITTTLLTNNTT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20509-96711
                     Sequence 13, Application PC/TUS9108177 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Highet, David W
REGISTRATION NUMBER: 30,265
REFRENCE/DOCKET NUMBER: 2050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4854
TELEPHONE: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein PCT-US91-08177-13
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                              20002
                                                                                                                                                                                                                                 CITY: Wash
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPOLOGY:
PCT-US91-08177-13
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                                                                                                                                                                                                                                                                                     COUNTRY:
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FRETIDES, POLYPEPTIDES, GLYCOPROTEINS, PREPIDES THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TRRATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 runinumunumininininnnumummunumuninnininnuminmumki
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12.2%; Score 188; DB 3; Length 216
Best Local Similarity 26.4%; Pred. No. 1.8e-09;
Matches 60; Conservative 23; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                      ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
                       APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PRETIDES, POLYPEPTIDES,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCES: ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEI/ NO. VEINY, Hana
RAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TRIPPONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-5EP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09588995A, Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 TTTTTTŤŤŤŤŤTTTTTŤ
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LENGTH: 216 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                     STREET: 385 SUCTIVE PAIO
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       GENERAL INFORMATION
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TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.4%; Score 222; DB 3; Length 37; larity 100.0%; Pred. No. 1.3e-13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT ARELCATION DATA:
APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 NKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 32
                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // Sequence 8, Application US/08928361B
// Patent No. 6071518
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Patent No. 6077511
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Antigenic por ITILE OF INVENTION: G-protein of ITILE OF INVENTION: G-protein of ITILE OF INVENTION: G-protein of UNDMBER OF SEQUENCES: 13 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DC SOFTWARE: Patentin Release #1.
                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-793-792-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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GENERAL INFORMATION:
APPLICANT: PETERSEN, CARCLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: MALSON, RICHARD C.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION NUMBER: US/09/58,995A
CURRENT APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/710,651
PRIOR PRILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOOFTWARE: PATENTIN Ver. 2.1
TANCHEL OF INVENTION OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF TANCH OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 IFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTTTTTTTT------TTTTTT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 ISQITIILASITPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 PNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 TKPTEEPTINTTKTNITTTLINNTTGNPKLTSOMETFHSTSSEGNLSPSQVSTTSEHPS 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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Best Local Similarity 22.7%; Pred. No. 3.5e-08;
Matches 70; Conservative 32; Mismatches 161; Indels 4
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                                                  REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEFRAME 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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; Patent No. 6514697
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ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                             LENGTH: 1837 amino acids
                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-3618-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 QPSSPPNTT 296
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                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-588-995A-5
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Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 TLTTAILQDAISQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTLLT 249
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TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
FILE REPERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PATENTIN UPF. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%; Score 188; DB 4; Length 216;
26.4%; Pred. No. 1.8e-09;
Live 23; Mismatches 120; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 NNTIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTI 296
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ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PETERS, VERNY, JONES & BIKSA
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Palo Alto
CA
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 216
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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| US-09-588-995A-5 | 8-995A-5 |
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| Query Match Best Local Matches 7 | Query Match 12.2%; Score 188; DB 4; Length 1837; Best Local Similarity 22.7%; Pred. No. 3.5e-08; Matches 70; Conservative 32; Mismatches 161; Indels 46; Gaps 5; |
| λ̈ | KTWDTLNHLLFIS |
| qq | 239 TGKTIPNTYAGVYRSNETKTTEPSANTNFLLVDPKINAPCNSENSFEQVQ 288 |
| λō | 53SLIITAIIPIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISPSNLSBI 107 |
| qu | 289 IFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTTTTTTTTTTTT 339 |
| ŏ | 108 ISQTITILASTIPGVKSNLQPITVKIKNTITIQIQPSKPITKORQNKPPNKPNNDFHFEV 167 |
| Пр | 340 TITITITITITITITITITITITITITITITITITITI |
| à | 168 FNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPT 227 |
| QQ | 398 TITITITITITITITITITITITITITITITITITITI |
| Š | 228 TKPTEEPTINITITILLTUNTTGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPS 287 |
| đđ | 458 TITITITITITITITITITITITITITITIKKPITTTITITIKKF 513 |
| Ğ | 288 QPSSPPWTT 296 |
| qa | 514 TTTATTTT 522 |

Search completed: October 29, 2003, 17:42:22 Job time: 17.3057 secs

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13-JAN-1994
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695.249 Million cell updates/sec
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                            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Respiratory Syncyt RSV G protein anti Peptide which indu Amino acid sequenc Human G protein, G Peptide which indu Human G protein, G Peptide which indu Human G protein, G Peptide which indu Human G protein, G RSV subgp. A prote

AAR95618
AAR44080
AAR44489
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Respiratory Syncyt RSV G protein anti Amino acid sequenc Human G protein, G

ALIGNMENTS

Amino acid sequence RSV G protein pept Streptococcal protein pept Streptococcal protein RSV subgroup A wil RSV subgroup A wil RSV sub-group A wil RSV G protein anti A GZNa peptide der Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence Amino acid sequence RSV subgroup A mod RSV

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AAR95612

PIV; RSV; multimeric; hybrid; pathogen; chimeric protein; vaccine. Multimeric hybrid genes and their chimeric proteins - are vaccines against multiple pathogenic infections e.g. syncitial virus (RSV) G protein. AAR39286 standard; Protein; 298 AA Respiratory syncitial virus 93WO-CA00001 92GB-0000117 (first entry) CONN-) CONNAUGHT LAB LTD. Ewasyshyn ME, Klein MH; (updated) WPI; 1993-243222/30. N-PSDB; AAQ45686 05-JAN-1993; 06-JAN-1992;

> Sequence of human HSRV glycoprotein HRSV glycoprotein Respiratory syncyt Secreted G protein Chimeric human res

AAR39286 AAW96313 AAP70845 AAR25302 AAW47605 AAW47605 AAW96314 AAW96314 AAB68336

100.0 91.8 91.8 91.8 79.6 6.64

Respiratory syncit Membrane bound G p

Description

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Query Match Length

Result No. 100.0

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containing the protein G sequence,
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                                         A novel multimeric hybrid gene is used as a vaccine. The gene consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza vitus (PIV) and respiratory syncitial vitus (RSV)). The gene sequences that are particularly used are those which encode PIV-3 F and MN proteins (AAQ45683, AAQ45684) and RSV F and (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                          241 TNITITLLTNNTIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 298
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                                                                                                                                                                   100.0%; Score 1544; DB 14; Length 298; llarity 100.0%; Pred. No. 2.6e-113; Conservative 0; Mismatches 0; Indels 0;
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para-influenza virus and respiratory syncytial virus
                     Claim 11; Figure 7A-7D; 80pp; English.
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tes 298; Conserv
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                                                                                                                                                                                                     vaccines by inserting the Title way. Figure in the control of alternative signal and expression sequences, for example the chimeric g protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences upstream of the G protein gene which enhance the G proteins immunoprotective ability. The resulting immunogenic composition will administered to a host organism the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly resulting in a balanced Thi/Th2 immune response and for raising Ab, by usual immunisation and cell fusion methods.
and
protective vaccines
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                                                                                                                                                                       The respiratory syncytial virus (RSV) G protein can be
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                                  to raise antibodies for diagnosis
                                                                                                      Claim 4; Fig 2; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                         1 MSKNKDQRTAKTLERTWDTLANHLLFISSCLYKLNLKSVAQITLSILAMIISTSLIIAAII
                                                                                                                              The sequences of mRNA encoding HRSV structural proteins are given in AAQ2622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
                                 Vaccines for human respiratory virus - include structural genes coding for native structural viral proteins and immunogenic fragments
                                                                                                                                                                                                                                                                         Score 1418; DB 13; Length 298;
Pred. No. 2e-103;
6; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.
                                                                                                 Disclosure; Page 18; 21pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory syncytial virus
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                                                                                                                                                                                                                                                                            91.8%;
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86US-0818740.
86WO-US02756.
92US-0897171.
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                                                                                                                                                                                                                                                                       Query Match 91.8
Best Local Similarity 93.3
Matches 278; Conservative
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                                                                                                                                                                                                                                             298 AA;
   N-PSDB; AAQ29623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-1986;
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                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TNIITTLLTSNTTGNPELTSQMETFHSTSSEGNPSPSQVSTTSEYPSQPSSPPNTPRQ 298
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                                                                                                                                        A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV vaccines. The vaccine can be administered to pregnant women or to women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age. (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K;
                                            Vaccines for human respiratory virus - comprising proteins or fragment encoded by a DNA sequence coding for human respiratory
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                                                                                                                                                                                                                                                                                      Match 91.8%; Score 1418; DB 8; Length 298; Local Similarity 93.3%; Pred. No. 2e-103; Nes 278; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                        14; Indels
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                                                                                                           Disclosure, Chart 13; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR25302 standard; Protein; 298
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88US-0218737.
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                                                                               syncytial virus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSRV glycoprotein G (gpG)
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WPI; 1987-206300/29
                                                                                                                                                                                                                                                        298 AA;
              N-PSDB; AAN70784.
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13-JUL-1988;
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03-MAR-1993
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PIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
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                                                                                                                                                                                                                                                                                                                                  1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                           Production of human respiratory syncytial virus glyco-protein F or (- by culturing eukaryotic host cells transfected with corresponding
                                                                                                                    The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein G (GpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare
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                                                                                                                                                                                                                                                                    DB 19; Length 298;
                                                                                                                                                                                                                                                                  Score 1418; DB 19; Length
Pred. No. 2e-103;
6; Mismatches 14; Indels
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                                                                                          Example 1; Columns 27-28; 17pp; English.
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                                                                                                                                                                                                        vaccines against HRSV.
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The invention relates to a recombinant Sendai virus comprising an exogenous nucleic acid encoding a paramyxovirus (PMV) protein or its antigenic fragment. The virus may be administered in combination with an antiviral chemotherapeutic compound. Two or more viruses expressing different PMV proteins nay be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PMV in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous nucleic acid encoding a second PMV protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering on or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral ceffective vaccine against PPIV or RSV (the major causes of paediatric effective vaccine against PPIV or RSV (the major causes of paediatric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory disease) and also to express any gene of interest in target calls, providing a positive medical impact on impaired cells. Wild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathalassaemia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The Sendai virus replicates at level that is high enough to induce sufficient immunity, but does not cause any harm to human recipient. The present sequence represents a respiratory synoyial virus (RSV) G protein (heavily glycosylated protein), a PMV protein ultable for expression by the recombinant virus of the invention.
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                                                              Recombinant Sendai virus useful in vaccines to protect infection paramyxoviruses, comprises exogenous nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.8%; Score 1418; DB 23; Length 298; 93.3%; Pred. No. 2e-103;
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                                                                                                             paramyxovirus protein or its antigenic fragment
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                                                                                                                                                         Disclosure; Page 48; 57pp; English
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WPI; 2002-130534/17.
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                       N-PSDB; AAS21045
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Gaps

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G protein; respiratory syncytial virus; RSV; recombinant vector;

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58.4%;
91.0%;
                                                                                                                                                                                                       87US-0137387.
                                                                                                                                                                          88WO-US03784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 91.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSQVSTTSE 284
                                 Chimeric polypeptide;
protein F; protein G;
                                                                                                                                                                                                                                                                                             WPI; 1989-206593/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSQVNISSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 AA;
                                                                                                                                                                                                                                  NHOPAN ( OF an)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200129054-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. frugiperda.
                                                                                                                                                                                                       23-DEC-1987;
                                                                                                              WO8905823-A
                                                                                                                                          29-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-2001
                                                                                                                                                                                                                                                                Wathen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB68336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB68336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSRITSQTTTLLASTTPGVKSNL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QPITVKTKNYTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRIPNKKPGKKTITIKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEBPTINTTKTTTT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                                                                                                                                                                                                                                                                                                                              The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein coproduced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences upstream of the G protein gene which enhance the G proteins immunoprotective ability. The resulting immunogenic composition will generate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly resulting in a balanced Th/772 immune response and for raising Ab, by usual immunisation and cell fusion methods. This truncated G protein is secreted since it lacks a transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT
                                                                                                                                                                                                                                                                                                        Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.6%; Score 1229; DB 20; Leason 10.0%; Pred. No. 1e-88; Indels
response; immunogenicity; tPA; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Preq. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP90441 standard; protein; 681 AA.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Fig 3; 67pp; English.
                                                                                                                                                                                                                               Li X, Sambhara S;
               tissue plasminogen activator
                                                                                                                                       98WO-CA00697.
                                                                                                                                                                    97US-0896442.
                                              Respiratory syncytial virus
                                                                                                                                                                                                (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
es 232; Conservative
                                                                                                                                                                                                                                                           WPI; 1999-132254/11.
N-PSDB; AAX08422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 AA;
                                                                                                                                     16-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1989
                                                                         W09904010-A1
                                                                                                                                                                                                                             Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP90441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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ID AAP
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AC AAP
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216 KPQTTKPKEVPTTKPTEEPTINTTKTNITTLLTNNTTGNPKLTSQMETFHSTSSEGNLS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490 QLGISPSNPSEITSQITTILASTTPGVKSTLQSTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 PNKPNNDPHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKKTTTKPTKKPTFKTTKKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 QLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 KPQTIKSKEVPTIKPTEBPINITIKINIITILLISNITIGNPBLISQMBIFHSISSEGNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Respiratory synctial virus; RSV; G-protein; annexin II; L-selectin;
RSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric polypeptide contg. a signal sequence and one or more immunogenic fragments from both human respiratory syncytial virus glycoproteins F and G. Can be used in vaccines. Hosts are, eg E. çoli, Chinese hamster ovary cells, murine C127 cells and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Chimeric human respiratory synctial virus glycoproteins F and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric human respiratory syncytial virus polypeptides(s) - contg. immunogenic fragments from HRSV glycoproteins F and G, for vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
                                                                  human respiratory syncytial virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 901; DB 10;
Pred. No. 2.1e-62;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of RSV G-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; page 47-48; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB68336 standard; protein; 299 AA.
                                                                                                                                                             Human respiratory syncytial virus.
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                                                                                                                                                                                                                                                                                                                                                                 61 FIISANHKVTLTTVTVQTIKNHTEKNITTYLTQVPPERVSSSKQPTTTSPIHTNSATTSP 120
                                                                                                                                                                                                                                                                                                                                                                                                    181 LCKSICKTIPSNKPKKKPTIKPTNKPTTNKRDPKTPAKTTKKETTTNPTKKPTLTT 240
                                                                                                                                                                                                                                                                                                                                                  FIASANHKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTP 120
                                                                                                                                                                                                                                                                                                                                                                                         121 GVKSNLQPITVKTKNTITTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                  TCWAICKRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPQTTKPKEVPTTKPTEEPTINTT 239
                                                                                                                                                                                                                                                                                                             ၀
                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                      1 MSKHKNQRTARTLEKTWDTLNHLIVISSCLYRLNLKSIAQIALSVLAMIISTSLIIAAII
                                                                                                                       Treatment of respiratory synctial virus infection (RSV) using Annexin
                                                                                                                                                                                                                                                                                                          1 MSKNKDQRTAKTLEKTWDTLNHLLFISSGLYKLNLKSVAQITLSILAMIISTSLIITAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 KTNITTILITNNTTGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 BRDTSTSQSTVLDTTTLEHTIQQQSLHSTTPENTPNSTQTPTASE-PSTSNSTQNT 295
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                        The specification describes a product which antagonizes binding of respiratory synctial virus (RSV) G-protein to annexin II or Lestectin, or causes a decrease in cell surface levels of annexin II or L-selectin. Such products are used in the manufacture of a medicament for use in prevention or treatment of RSV infection. The present sequence represents a RSV G-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carrier; G protein; RSV; cancer.
                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSV G protein peptide G2Na and diphtheria anatoxin peptide DTb.
                                                                                                                                                                                                                                                                    Length 299;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                 Query Match
49.9%; Score 771; DB 22;
Best Local Similarity 54.7%; Pred. No. 1.3e-52;
Matches 162; Conservative 36; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diphtheria anatoxin; immune response; antigen; hypersensitivity response; vaccine; infection;
                                                                                                                                                    Disclosure; Page 71-73; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP97862 standard; protein; 361
                                                                                                                                   II or L-selectin derivatives
                    23-OCT-2000; 2000WO-GB04084.
                                        99GB-0024990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-2001; 2001FR-0009733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                          (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syncytial
                                                                               Bird M;
                                                                                                   WPI; 2001-316238/33
                                                                                                                                                                                                                                              299 AA;
                                        21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR2827606-A1
                                                                               Malhotra R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-2003
26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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PNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKP---GSINLDMDVIRDKTKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a fusion protein comprising a peptide derived from the G protein of Respiratory syncytial virus (RSV) linked to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition; RSV; RSV infection; lung; respiratory tract; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTIN------TTKT
                                                                                                                                                                                                                                                              New peptide derived from diphtheria anatoxin, useful as carrier in vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a fusion protein of P40 and RSV antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | | : | | | : | | 121 KIESLKEHGPIKUKMSESPNKTVSEEKAKQYLEEFHQTALE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 NITT-----TLINNITGNPKLTSQMETFHSTSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.6%; Score 580; DB 24;
70.8%; Pred. No. 1.6e-37;
tive 5; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against infectious agents or tumour cells.
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 27-28; 42pp; French
                                                                 (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virue
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20-JUL-2001; 2001FR-0009733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 114; Conservative
                                                                                                                                  Nguyen NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klebsiella pneumoniae.
Respiratory syncytial
                                                                                                                                                                                             WPI; 2003-241969/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VO200121203-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1999;
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Klebsiella
                                                                                                                                  Corvaia N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Length 291;

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The present sequence represents a fusion protein comprising a peptide derived from the G protein of Respiratory syncytial virus (RSV) linked to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria residue, are useful as carrier peptides. Deletion of Cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells.
                       Disclosure; Page 26-27; 42pp; French.
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 67.1
Matches 110; Conservative
                                                                                                                                                                                                                                                                       291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ----
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                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                    130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP97863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
          XXX888888888888888888
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                                                                                                                                                                           The present sequence represents a fusion protein comprising a Klebsiella pneumoniae outer membrane protein A (OmpA) designated P40 and a respiratory syncytial virus (R8V) antigen. Enterobacterium OmpA proteins, a ssociated with an immunogenic peptide from R8V are used to prepare a nasal composition that induces a protective response, against R8V infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing vaccines for prevention or treatment of R8V infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPCKKTTTKPTKKPTFKT 210
                                                                              Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAPDRRVEIEVKGYKEVVTQ-----PQGPG-----DPMTVKTKNTTTTQTQPSKPTTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTQDPQLGISFSNLSELTSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQ
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vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carrier; G protein;
RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
37.1%; Score 572.5; DB 22; Length 452;
Best Local Similarity 76.1%; Pred. No. 8.2e-37;
Matches 108; Conservative 5; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSV G protein peptide G2Na and diphtheria anatoxin peptide DTa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diphtheria anatoxin; immune response; antigen; hypersensitivity response; vaccine; infection;
                                                                                                                                              Example 2; Page 31-32; 39pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKKDLKPQTTKPKEVPTTKPTE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP97861 standard; protein; 291 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium diphtheriae.
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 Corvaiea N, Goestch
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                                                                                                                                                                                                                                                                                                                                              452 AA
                                             N-PSDB; AAF80153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                            Sequence
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PNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKPGSGADDVVDSSKSFV--- 119
                                                                                        4 TVKTKNITITIQIQPSKPITKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWALCKRI
                                                                                                                             190 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTE--EPTINTTKTNITTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a fusion protein comprising a peptide derived from the G protein of Respiratory syncytial virus (RSV) linked
                                                              TVKTKUTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAICKRI
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide derived from diphtheria anatoxin, useful as carrier in
Vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                            RSV G protein peptide G2Na and diphtheria anatoxin peptide DTaDTb.
                                     23;
                                                                                                                                                                                                                              ----MENF---SYHGTKPGYVDSIQKGIQKPKS 146
                                  21; Indels
                                                                                                                                                                                            248 LINNITGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSS 291
 DB 24;
36.6%; Score 564.5; DB 67.1%; Pred. No. 2e-36; tive 10; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 29-30; 42pp; French
                                                                                                                                                                                                                                                                                                             ABP97863 standard; protein; 548 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Respiratory syncytial virus.
Corynebacterium diphtheriae.
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                                                                                                                                                                                                                                                                              PNKKPGKKTTTKPTKKPTFKTTKKOLKPQTTKPKEVPTTKPTE--EPTINTTKTNITTL 247
                                                                                                                                                                                                                                                                                             64 PNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKSVPTTKPGSGADDVVDSSKSFV---- 119
to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells.
                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                          TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRI
                                                                                                                                                                                                                            130 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVPVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus; protein G; carrier protein; immunogenicity; increase; enhance; vaccine; anti-viral; human serum albumin; binding; immunostimulation; respiratory syncytial virus; fusion protein.
                                                                                                                                                                                                 23;
                                                                                                                                                                       Query Match 36.6%; Score 564.5; DB 24; Length 548; Best Local Similarity 67.1%; Pred. No. 4.4e-36; Matches 110; Conservative 10; Mismatches 21; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcal protein G fragment BB fused to RSV hapten G2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                  248 LINNTIGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSS 291
                                                                                                                                                                                                                                                                                                                                                         Stahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enhancing immunogenicity by coupling immunogen to serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nygren PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "residues 130-230 of RSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nguyen Ngoc T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric Streptococcus sp. Chimeric Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAR95660 standard; Protein; 349
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/label= G2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-FR01466
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/label= BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94FR-0013310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-251766/25
                                                                                                                                                548 AA;
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                                                                                                                                                Sequence
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                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aliphatic ammonium salt; immunogen; antigen; syncytial virus infection; G protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of fusion protein comprising 2 G protein fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                    216 NGKTLKGETTTEAVDAATARSFNFPILENSM---TVKTKONTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                               103 NLSEITSQTTT--ILASTT----PGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of quaternary aliphatic ammonium salt and immunogen or antigen to combat respiratory syncytial virus infections
                                                                                                                                                                                                                                                                                                                                                               Gaps
albumin-binding protein - useful for preparing improved vaccines, e.g. against Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                        Length 349;
                                                                                                                                                                                                                                                                                                                    Query Match 36.4%; Score 562; DB 17; Length 3
Best Local Similarity 78.1%; Pred. No. 4e-36;
Matches 107; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "G protein fragment of VRS"
                                                        Disclosure; Page 81-83; 102pp; French
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Respiratory syncytial virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-267782/28.
                                                                                                                                                                                                                                                                                   349 AA;
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                                                                                                                                                                                                                                                                                     Sequence
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The specification describes a method which uses quaternary aliphatic ammonium salts together with an immunogen or antigen to treat syncytial virus infections. The combination of the salt with the antigen or immunogen improves immunogenicity and equilibrates the Th1/Th2 immune response. The method is used for the treatment of respiratory syncytial virus infections. The present sequence represents a fusion protein, comprising an albumin binding domain of the G protein of Streptococcus sp. fused to a G protein fragment of respiratory syncytial virus (VRS, long version). The fusion protein is used as an antigen in the method of the invention. Claim 16; Page 22-23; 35pp; French.

349 AA; Sequence

103 NLSEITSOTTT--ILASTT----PGVKSNLQPTTVKTTKNTTTTQTQPSKPTTKQRQNKP 155 156 PNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKXDL 215 273 PNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKKTTTKPTKKPTFKTTKKDH 332 Query Match 36.4%; Score 562; DB 22; Length 349; Best Local Similarity 78.1%; Pred. No. 4e-36; Matches 107; Conservative 10; Mismatches 10; Indels 10; Gaps g à Db ð

Search completed: October 29, 2003, 17:38:00 Job time: 70.034 secs

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AL071370 Drosophil
EX443342 EX443342
EX385076 EX385076
AL102202 Drosophil
AL068607 Drosophil
BX436853 EX436853
AL135357 Pen trogl
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AL548181 AL548181
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACK14B09 of RPCI-98 library from Drosophila melanogaster (fruit
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Modotterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
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EX436369 GI:30787529 EX436369.1 GI:30787529
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1180)
                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODAO11BE07QP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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             Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
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16.8%; Score 120; DB 29; Length 895;
Best Local Similarity 25.0%; Pred. No. 1.3e-09;
Matches 129; Conservative 186; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 308 others
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Totoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Hatanabe, H. and Sakaki, Y.
Direct Submission

Bubmitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
submitted (2-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKBN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                  GSS 04-NOV-2001
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                                                                                                      MALZ/412
Pan troglodytes DNA, clone: PTB-138R06.R, genomic survey sequence.
AG127412
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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Llarity 46.6%; Pred. No. 3.3.e-07;
Conservative 0; Mismatches 374; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
: 35I c 31 g 23 t 36 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-138E06.R"
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Pan troglodytes
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          612 AAAAAGHYYNTKHHYTYY
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Matches
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AG127412
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                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed
with a NotL-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
154 c 191 g 420 t 288 others
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BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr ww.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 516.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001BG06Opl&cluster=516.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001BG06Opl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.6%; Score 111.4; DB 13; Length 1180; 25.8%; Pred. No. 2.6e-08; tive 194; Mismatches 219; Indels 1;
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP001YM12"
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                                                              Contact: Genoscope
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Tetracdon nigroviridis genome survey sequence T7 end of clone 104P14 of library G from Tetracdon nigroviridis, genomic survey
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : Begref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGC 360
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Tetracdon nigroviridis

Tetracdon nigroviridis

Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopteryqi; Neopteryqii; Teleostei; Buteleostei;

Acanthomorpha; Acanthopteryqii; Percomorpha; Tetracdontiformes;

Tetradontoidea; Tetracdontidae; Tetracdon.
                                                                                                                                                                                                         241 ACTACAAAACAACGCCAAAACAAACCACCAAACAAACCAATAATGATTTTTCACTTCGAA 300
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                                                                                                                                                                                                                                                                                                                                                                                      361 AAAAGAATACCAAAAAAAAACCAGGAAAGAAAACCACCACCAAGCCTACAAAAAACCA
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Characterization and repeat analysis of the compact genome of EreBhwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
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                                                                           Length 922;
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Nat. Genet. 25 (2), 235-238 (2000)
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Determination of this BAC-ena.fr)
Determination of this BAC-ena sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Rosewell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST library is more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.from.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA linear GSS 03-JUN-1999 survey sequence TET3 end of BAC # com Drosophila melanogaster (fruit
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ACCCTGCAGCATATGCAGCAACAACCTGCTGGGCTATCTGCAAAAGAATACCAAA
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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BACR14D09 of RPCI-98 library from Drosophila melanogaster
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Ephydroidea; Drosophilidae; Drosophila
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14D09"
/clone lib="RPCI-98"
/note="end : TET3"
a 95 c 109 g 221 t 274 ot
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AL066784
AL066784.1 GI:4945247
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/woltrpe="mina" and sapiens"
/wol type="mina" and sapiens"
/db xref="caxon:9606"
/clone="CSODG004YF15"
/tissue type="mina" and sapiens B CELLS (RAMOS CELL LINE)"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCWVSPORT 6; lst strand cDNA was primed with a Not1-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and CEORV sites of the pCWVSPORT 6 vector.
Library was not normalized." however
 Contact: Genoscope
Genoscope
Genoscope
Genoscope
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - This sequence belongs to sequence cluster
8262.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG004CC08NP1&cluster=8262.f. Contact :
Feng Liang Email : fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG004CC08NP1.
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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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CELLS (RAMOS CELL LINE) Homo sapiens cDNA
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46.0%; Pred. No. 9e-07;
ive 36; Mismatches 222; Indels
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                                                                                                               /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 191066 EWRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BAGs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutcyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
BCORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2, cn bw sp, the ame strain used for the BDGP's
Pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACRAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR3219 of RPCI-98 library from Drosophila melanogaster (fruit AL071370.
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                                          541 CTGCTCACCAACACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ehydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                 13.8%; Score 99; DB 29; Length 1101; 25.6%; Pred. No. 2.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BARR3C19"
/clone lib="RRC19"
/note="end : TET3"
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AL531977 Homo sapiens FETAL LIVER Homo sapiens CDNA clone CSODM003YD03 5-PRIME, mRNA sequence.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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BP 191 91006 EVRY cedex - France
Bmail: sequefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8045.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/
cgi.bin/cluster.cgiseq=CSODM003CB02QPl&cluster=8045.f. Contact
cgi.bin/cluster.cgiseq=CSODM003CB02QPl&cluster=8045.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http:/fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODM003CB02QPl.
Location/Qualifiers
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14.0%; Score 99.8; DB 9; Length 1201;
Best Local Similarity 41.7%; Pred. No. 1.7e-06;
Matches 223; Conservative 52; Mismatches 260; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                  LI,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-Length cDNA libraries and normalization Unpublished
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                                                                                                                                                AL531977.2 GI:31069809
                                                                                                                                                                                           sapiens (human)
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Contact: Genoscope
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BP 1919 91006 EVRY cedex - Prance
BP 1919 91006 EVRY cedex - Prance
Inbrary was constructed by Life Technologies, a division of
Invirogen. This sequence belongs to sequence cluster 4073.r For
more information about this Gluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgirseq=CSODL006BC06ND1&cluster=4073.r. Contact:
Feng Liang Email : fliangelifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODL006BC06NP1.
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BX385076 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED HOMO Sapiens CNDA clone CSODL006YEL2 3-PRIME, mRNA sequence.
                                                                                                149 CTTCAACAACAACCAGGAGTCAAGTCAAACCTGCAACCCCACAACAGTCAAGACTAAAAACA 208
                           89 AGCTIGGAAICAGCTICTCCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAG 148
                                                                                                                                                                                                                                                                                        389 AGRAPACCACCACCARGAGCTACAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCA 448
                                                                                                                                                                                                                                                                                                                                                                 449 AACCTCAAACCACTAAACCAAAGGAAGTACCCACCACCAAGCCCACAGAAGAGCCAACCA 508
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1100)

                                               269 CAAACAAACCCAATAATGATTTTCACTTCGAAGTGTTTTAACTTTTGTACCCTGCAGCATAT
                                                                                                                                        633 MMINAMMINIHIGNTINININININIMERINGNTINININTININAMMININIMMAMMAMMINININ
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                                                                                              into
                     453 TCAAACCACTAAACCAAAGGAAGTACCCACCACCAAGGCCCACAGAAGAGCCAACCATCAA 512
CAPACCCAATAATGATTTTCACTTCGAAGTGTTTTAACTTTGTACCCTGCAGCATATGCAG 332
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 753)
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BP 191 91006 EVRY cedex - France
Bmail: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3806.r For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.genoscope.cns.fr/
cgi.bin/cluster.gi?seq=CSODH001DC02NP1&cluster=3806.r. Contact
Feng Liang Email: fliang@lifeten.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODH001DC02NP1.
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

29 c 99 g 264 t 308 others
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                                                                                                                                                                                                                                                                                                    513 CACCACCAAAACAACATCACAACTACACTGCTCACCAACAACACC 558
                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"

(db_xref="taxon:966"

(db_xref=SOBHOO11YF04"

(tissue_type="T_CELLS (JURKAT_CELL_LINE)"

(cell_line="UURKAT_CELL_LINE"
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1035
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Best Local &
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                                                                                                                                                                                                                        BASE COUNT
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CNS009KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

175 c 126 g 196 t 170 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 TCAAACCTCAAACCACTAAACCAAAGGAAGTACCCACCACCACCACAGAAGAGCCAA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                 791
                                                                                                                                                                                                                                                                                                                                                                                               266 CACCAAACAAACCAATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                           911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851
                                   COT 25-NORMALIZED"
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(EDGP)
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                                                                                                                                                                                                                                                                                                                                                                                                                 732 ААААМААААААМИСААААААААААААААААСКАСИМИАААААМАМАМАМИАА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGCTTCAACACACCAGGAGTCAAGTCAAACCTGCAACCCCACAACAGACTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome Burvey sequence SP6 end of BAC BACN08M09 of DrosBAC library from Drosophila melanogaster (fru fly), genomic survey sequence.

AL102202
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Bandoterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                              /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMAL
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as collaboration with the Buropean Drosophila Genome Project
                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                          Length 1100
                                                                                                                                                                                                      13.5%; Score 96.2; DB 13; Length 38.9%; Pred. No. 6.5e-06; ive 72; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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                 clone="CSODL006YE12"
db xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL102202.1 GI:5613813
                                                                                                                                                                                                                                     Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
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                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                        Best Local
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                         BASE COUNT
ORIGIN
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CNS012Z4/c
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AUTHORS
TITLE
JOURNAL
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http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 CHIMICACACAAACCAMCMACAMACAAACAMAMAAACACCTAAAMACACCMMACACMAACACM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGCAAAAGAATACCA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 TITITITITYYTTTACAMNCACWACAWCTYMCATAAATWWWCAMACACAYWACCCATCWYH 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791 bp DNA linear GSS 03-JUN-15 Drosophila melanogaster genome survey sequence T7 end of BAC #BACR19F04 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACAACCCCAACATAC
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                                                                                                                                                                                                                                                                                                                                                                             Length 1097;
                                                                                                                                                                                                                                                                                                                                                                                                                    199; Conservative 119; Mismatches 290; Indels
                                                                                                                                                                       melanogaster"
                                                                                                                                                                                                                                                                                                                                                                           DB 29;
                                                                                                                                                                                                                                                                                                                                                                         Score 95.8; DB 29
Pred. No. 7.6e-06;
                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                 398
                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="bacNoBM09"
/clone lib="brosBAC"
/plasmid="pBeloBAC11"
                                                                                                                                           1. .1097
/organism="Drosophila
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 196 g
                                                                                                                                                                                                                                                                                              . SP6"
                                                                                                                                                                                                                                                                                                                                                                           13.4%;
32.7%;
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119 c
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                  pBeloBAC11
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us-09-462-816-3.rst

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CNS00LOO 1101 bp DNA linear GSS 03-JUN-1999 Prosophila melanogaster genome survey sequence TET3 end of BAC:
BACK32D02 Of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 MAYCMYCCMCYTTCMCCMAHHTWAMACAMTMWAHACHTHTHWCMTMTTWATMTCMMCAHT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635 MAHTMYTMAMCHAAHNWTTWTMMMENAYAHCACWWTTMCAMMONWCAAMCMHMMMMMA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 695 MHTANTCACMMAANMAMMTWWAMMACMRMAMMCCCSCAMMCMAMAAHWMACMA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 GAGTCAAGTCAAACCTGCAACCCACAAAGGTCAAGACTAAAAACACAACAACAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 TCTCCAATCTGTCTGAAATTACATCACAAACCACCATACTAGCTTCAACAACACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 TCTCCCTCAYTTCTBCCTTTCMCTCMCACMACHCTCHCMCTCYVMCACYATCMMHAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 ATGATTITCACTICGAAGIGITIAACTITIGIACCCIGCAGCAIAIGCAGCAACAATCCAA
                                                                                                                                                                                                                                                                          Drosophila melanogaster
Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.3%; Score 95; DB 29
18.5%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 t
                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="BACR32D23"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                    AL068607.1 GI:4958689
                         445 AACACACAAATAAAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 c
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                                                                                                                                                                                                                                                                                                                                                                         Genoscope
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Best Local 8
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
                                                                                                                                         DEFINITION
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AUTHORS
                                                                                 RESULT 14
CNS00LO0
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                                                                                                                                                                                                  Dispect submissions.

Submisted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruiffy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 CAAACCCA-ATAATGATTTTCACTTCGAAGTGTTTAACTTTGTACCCTGCAGCATATGCA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACCACCACCAAGCCTACAAAAAACCAACCTTCAAGACAACCAAAAAAGATCTCAAAC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAAACCACTAAACCAAAGGAAGTACCCACCACCAAGCCCAACGAAGAGCCAACCATCA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACCACCAAAACAAACATCACAATTACACTGCTCACCAACAACACCACACGGAAATCCAA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
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/note="end : T7"
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Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5355.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0CAP003DF06NP1&cluster=5355.r. Contact:

Feng Liang Bmail: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ Invitrocen Corporation 1600

Faraday Avenue Genoscope sequence ID: CS0CAP003DF06NP1.
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/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
122 others
139 c 79 g 53 t 122 others
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BX436853 Homo mapiens THYMUS Homo mapiens cDNA clone CSOCAP003YL12
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1 (bases I to 899)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                    CAAACATCACAACTACACTGCTCACCAACACACCACAGGAAATCCAAAACTCACAAGTC
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llarity 43.6%; Pred. No. 1.2e-05;
Conservative 62; Mismatches 227; Indels 3
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Search completed: October 30, 2003, 01:15:25 Job time : 1946.71 secs

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Sequence 1, Application US/09847173
Publication No. US20020182228A1
GENERAL INFORMATION:
APPLICANT: Collins, Peter L.
TITLE OF INVENTION: PRODUCTION OF INFECTIOUS RESPIRATORY
SYNCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES
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CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Crew LLP
STREET: Townsend and Townsend and Crew LLP
STREET: Townsend and Townsend and Crew LLP
CITY: San Francisco
STRATE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STRATE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STRATE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
CONDUTE: Two Embarcadero Center, 8th Floor
COMPUTER READABLE FORM:
MEDIUW TYPE: Floopy disk
COMPUTER: IBM PC compatible
OMPUTER: Floopy disk
COMPUTER: Floopy disk
FILING DATE: 03-May-2001
CLASSIFICATION NUMBER: 04-000
REPERENCE/DOCKET NUMBER: 15-280-250-1
TELECOMMUNICATION:
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LENGTH: 15223 base pairs
TYPE: nucleic acid
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TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 1:
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Sequence 20723, A Sequence 2004, Ap Sequence 1893, App Sequence 165, App Sequence 165, App Sequence 1931, Ap Sequence 20131, Ap Sequence 20131, Ap Sequence 20131, Ap Sequence 2013, Ap Sequence 2013, Ap Sequence 2013, App Sequence 201, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 327, Appl Sequence 327, Appl Sequence 327, Appl Sequence 327, Appl Sequence 327, Appl Sequence 327, Appl Sequence 217, Appl Sequence 217, Appl Sequence 217, Appl Sequence 217, Appl Sequence 258, Appl Sequence 217, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Appl Sequence 26582, Ap
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    \begin{array}{c} 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\
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691
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Best Local Similarity 95.3
Matches 470; Conservative
                                       COUNTRY: U.S.A.
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                                                   ZIP: 10036
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                                                                                     Score 654.8; DB 10; Length 15223;
Pred. No. 4e-164;
0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Briles, David E.
McDaniel, Larry S.
Curiel, David T.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
ADMINISTERING PNEUMOCOCCAL DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: other
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-847-173-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/09844645; Patent No. US20020102242A1; GENERAL INFORMATION:
                                                                                    Query Match
Best Local Similarity 94.8%;
Matches 677; Conservative
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US-09-844-645-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Pc-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 445.8; DB 10;
Pred. No. 5.8e-109;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                    NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2450
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,505
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                      7 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) 5 SEQUENCE DESCRIPTION: SEQ ID NO: US-09-844-645-4
                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 840-3333
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 2, Application US/10312841
| Publication Wo. US20030186277A1
| GENERAL INFORMATION:
| APPLICANT: Epigenomics AG
| TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des |
| FILE REFERENCE: BO1/1208/WO |
| CURRENT APPLICATION NUMBER: US/10/312,841 |
| CURRENT PILING DATE: 2002-12-30 |
| NUMBER OF SEQ ID NOS: 2
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5548 TCTACATCAAATTCCACCCAAAATACCCAATCACATGCTTAGTTATTCAAAAACTACA 5605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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12.0%; Score 85.8; DB 12;
Best Local Similarity 47.0%; Pred. No. 3.1e-11;
Matches 334; Conservative 0; Mismatches 372;
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ORGANISM: Artificial Sequence
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US-10-312-841-2
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; Sequence 10, Application US/09827688
; Publication No. US20030165476A1
; GENERAL INFORMATION:
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ORGANISM: RSV
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US-09-827-688-10
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APPLICANT: OLEK, Alexander
APPLICANT: DLEX, Alexander
APPLICANT: BIEDENBROCK, Christian
APPLICANT: BIEDENBROCK, Christian
APPLICANT: BIEDENBROCK, Christian
APPLICANT: BIEDENBROCK, Christian
APPLICANT: BIEDENBROCK, Christian
APPLICANTON: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR PELING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
SEQ ID NOS: 2424
SEQ ID NOS: 2424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTGCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 TACAAAACAACGCCA--AAACAAACCACCCAAACAAACCCAATAATGATTTTCACTTCGAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 82.6; DB 12; Length Pred. No. 1.4e-11; 0; Mismatches 294; Indels
   160 CACCAAACCACGCAAACAACAAAC 131
                                                                                                             ; Sequence 1076, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 289; Conservative
                                                                                            US-10-311-455-1076/c
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                                                                                                               Sequence 4304, Application US/09878574

Sequence 4304, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Number: 0209/878,574

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT PELICATION NUMBER: 09333,535

PRIOR FILING DATE: 1990-06-14

NUMBER OF SEQ ID NOS: 15775

LENGTH: 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 IGCAACCCACAACAGICAAGACTAAAAACACAAACAAACACAAACACAAACACAGCAAGC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581
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                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 793;
Query Match
11.7%; Score 83.6; DB 10; Length 'Best Local Similarity 48.4%; Pred. No. 2.7e-12;
Matches 276; Conservative 0; Mismatches 292; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure

: LOCATION: (1)...(793)

: OTHER INFORMATION: unsure at all n locations

: OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-C11

18-09-878-574-4304
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Glycine max
                                                                                      RESULT 5
US-09-878-574-4304/c
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109 AATCTGTCTGAAATTACATCACAAACCACCATACTAGCTTCAACAACACCAGGAGTC 168
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FRATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       ### AFFLICAMY: NULT.

| TITLE OF INVENTION: Diagnosis of Diseases Associated with TITLE OF INVENTION: Metastasis |
| FILE REPERENCE: 5013.1007 |
| FILE REPERENCE: 5013.1007 |
| CURRENT APPLICATION NUMBER: US/10/240,485 |
| CURRENT FILING DATE: 2002-10-62 |
| PRIOR PILING DATE: 2000-04-06 |
| PRIOR APPLICATION NUMBER: DE 10019058.8 |
| PRIOR APPLICATION NUMBER: DE 10019173.8 |
| PRIOR PILING DATE: 2000-04-06 |
| PRIOR PILING DATE: 2000-04-07 |
| PRIOR APPLICATION NUMBER: DE 10019173.8 |
| PRIOR PILING DATE: 2000-06-07 |
| PRIOR PILICATION NUMBER: DE 10043826.1 |
| PRIOR PILICATION NUMBER: DE 10043826.1 |
| PRIOR PILICATION NUMBER: 2000-09-01 |
| NUMBER OF SEQ ID NOS: 202 |
| SEQ ID NOS: 202 |
| PRIOR FILING DATE: 2000-09-01 |
| NUMBER OF SEQ ID NOS: 202 |
| PRIOR FILING DATE: 2000-09-01 |
| NUMBER OF SEQ ID NOS: 202 |
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| PRIOR FILING DATE: 2000-09-01 |
| PRIOR FILING DATE: 2000-09-01 |
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Pred. No. 4e-11;
0; Mismatches 269;
                                                                                                                                                  5386 AAAAAAAAAATAAAATCTCCTCC
                                                                                               589 GAAACCTTCCACTCAACCTCCTCC
                                                                                                                                                                                                                                                                            Sequence 82, Application US/10240485
Publication No. US20030148327A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 46.65
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: unsure
; LOCATION: (5837..)
US-10-240-485-82
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                                                                                                                          US-10-311-455-1056/c

Sequence 1056, Application US/10311455
Publication No. US20030143606A1
Sequence 1056, Application US/10311455
Publication No. US20030143606A1
SENERAL INFORMATION:
APPLICANT: DIERNANCY, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
FILE REPRENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
SRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       506 AACCITITACCCAAACCCCATIACAICAICACCTAAACCICTACCAAACCIAA 5447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 AATCTGTCTGAAATTACATCACAAACCACCATACTAGCTTCAACAACACCAGGAGTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 CCCAGCAAGCCCACTACAAAACAACGCCAAAACAAACCAACAAACCAAAACCAATAATGAT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 TITCACTICGAAGIGITIAACTITGIACCCIGCAGCAIAIGCAGCAACAACCAGC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 ACAAAAAACCAACCTTCAAGACAACCAAAAAAATCTCAAACCTCAAACCACTAAACCA 468
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5570, 5573, 5577..5578, 5592, 5732
c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.4%; Score 81.4; DB 12; Length 16167;
Best Local Similarity 46.6%; Pred. No. 4e-11;
Matches 235; Conservative 0; Mismatches 269; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 5837..5838
COTHER INFORMATION: n is a or g or c or US-10-311-455-1056
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is a or g or
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ORGANISM: Artificial Sequence
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LOCATION: 4003, 5529,
OTHER INFORMATION: n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 ACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTGCAA
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Best Local Similarity 46.5%; Pred. No. 7.8e-11;
Matches 264; Conservative 0; Mismatches 302; Indels 2;
                                                                                                                                                                                          ; sequence 1981, Application US/10017161
; bublication No. US20030143668A1
; bublication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAXIKO
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ARIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT PILING DATE: 2001-246789
; PRIOR PILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SEQ ID NO 1981
; SEQ ID NO 1981
; LENGTH: 1972
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LOCATION: (1319)..(1328)

OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1981
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                                                                                                                2931 AAAAACAAAAAAAAAACAAA 2912
                                                                            573 ACTCACAAGTCAAATGGAAA 592
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LOCATION: (975)..(994)
OTHER INFORMATION: a, t,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1)..(1972)
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LOCATION: (1)..(
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NAME/KEY: CDS
LOCATION: (201
FEATURE:
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                                                                                                                                                                                                                                                                             Sequence 1670, Application US/10311455
Publication No. US20030143606A1
ABPLICANT: USER, Alexander
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Paper
                                 5506 AACCTTTTACCCAAACCCCATTACATCACCCTAACCTAAACCTCTACCAAACCTAA 5447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 AACAACACCAGGAGTCAAGTCAAACCTGCAACCCACAACACAGACTAAAAACACAAC 212
529 ATCACAACTACACTGCTCACCAACAACACCCACAGGAAATCCAAAAACTCACAAGTCAAATG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 AACCACCACCAAGCTACAAAAAAACCAACCTTCAAGACAACCAAAAAAGGATCTCAAAACC 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
SRIOR FILING DATE: 2000-09-01
SRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure; LOCATION: 1936; OTHER INFORMATION: n is a or g or c or t US-10-311-455-1670
                                                                                                                                                                                      5386 AAAAAAAAAATAAATCTCCTCC 5363
                                                                                                                                                   589 GAAACCTTCCACTCAACCTCCTCC 612
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Sequence 2109. Application US/09983965

Patent No. US20020137160A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Tao, Nengbing

APPLICANT: Tao, Nengbing

APPLICANT: Tao, Nengbing

APPLICANT: Tao, Nengbing

APPLICANT: Tao, Nengbing

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILLE OF INVENTION: WINSCILE AND FAT DEPOSITION

FILLE OF INVENTION: WINSCILE AND FAT DEPOSITION

FILLE OF INVENTION: UNBER: US/09/983, 965

CURRENT APPLICATION NUMBER: US 99/465,231

PRIOR FILING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 5912

FEACULE OF SEQ ID NOS: 5912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 CAACCITCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGIAC 478
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                                                        196 CCACCCCAAAAACAAACACCCCAACCACAAAACAAA 150
                              545 TCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76.4; DB 10; Length
Pred. No. 1.9e-10;
0; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (335)
CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION: Clone ID: 34-LIB3057-015-Q1-K1-A6
US-09-983-965-2109
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Best Local Similarity 47.9%;
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: unsure
                                                                                                                         RESULT 12
US-09-983-965-2109/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR PRILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
484 ACCAAGCCCACAGAAGAGCCAACCATCAACACCAACAAAAAAACAACAACTACACTG 543
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                                                                                                                   544 CTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCACTCA
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ilarity 50.9%; Pred. No. 1.7e-10;
Conservative 0; Mismatches 199;
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COTHER INFORMATION: unsure at all n locations
COTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-G1
US-09-878-574-4296
                                                                                                                                                                                                                                                                                                                  1345 CCACCACCATCACCACCACCATCACCAC 1372
                                                                                                                                                                                                                                                                         CAACCCTCATCTCCACCCAACACAC 691
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Patent No. US20020110548A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 207; Conserva
                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-878-574-4296/c
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LENGTH: 576
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Sequence 4312, Application US/09878574

Sequence 4312, Application US/09878574

Batent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/33,535

PRIOR PLING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

LENGTH: 577
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413 CACARCACARACONARÁCACACACARACARACACACACACACACACACACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 TTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGCAAAAGAATA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAA 592
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CTHER INFORMATION: unsure at all n locations
CTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-G11
US-09-878-574-4312
                                                                140 CNANNNANNNCNNNGANNACCNANACANNAC 110
                              661 TCACAACCCTCATCTCCACCCAACACACAC 691
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
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NAME/KEY: unsure
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US-10-311-455-675/c
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                   Sequence 4306, Application US/09878574

Batent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: In Rosa, Thomas J.

APPLICANT: In Rosa, Thomas J.

APPLICANT: In Rosa, Thomas J.

APPLICANT: In Rosa, Thomas J.

APPLICANT: In Rosa, Thomas J.

TITLE OF INVENTION: Michael D.

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/933,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR PLIING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 4306
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                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(1030)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-D11
                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Glycine max
          JS-09-878-574-4306/c
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
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US-09-878-574-4306
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Sequence 675, Application US/10311455
Publication No. US2003014366A1
GENERAL INFORMATION
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dispansis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Dispansis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Dispansis of Diseases
FILE REFRENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 675
LEAST OF SEQ ID NOS: 2424
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10.5%; Score 74.8; DB 12; Length 6089;
Best Local Similarity 53.6%; Pred. No. 1.5e-09;
Matches 178; Conservative 0; Mismatches 152; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5778 CAATCCCCCTAAACACCGAAACAAAAC 5747
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ORGANISM: Artificial Sequence
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Search completed: October 30, 2003, 03:23:54 Job time : 246.957 secs

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Sequence 7, P
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1: /cgT2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgT2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgT2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgT2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgT2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgT2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequence 1, A Sequence 77, Sequence 77, Sequence 3, A

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| | 207.6 207.6 207.6 207.6 207.6 207.6 201.2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | HESULT 1 UG-08-467-963C-7 Sequence 7, Application Patent No. 5968776 GENERAL INPORMATION: APPLICANT: EMASYSHY TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TOTALS OF INVENTION: TOTALS OF INVENTION: MEDIUM TYPE: FIDOR COMPUTER READABLE FO MEDIUM TYPE: FIDOR COMPUTER READABLE FO MEDIUM TYPE: FIDOR COMPUTER READABLE FO MEDIUM TYPE: FIDOR COMPUTER READABLE FO MEDIUM TYPE: FIDOR MEDIUM T | ; ; TOPOLOGY: linear US-08-467-963C-7 |

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CORPERATIOG SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION: A35
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-ADN-1993
FRICK APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
RELING DATE: 06-ADN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-687 MIS:jb
TELEGOMMUTCATION INFORMATION:
TELEFAKE (416) 595-1155
TELEFAKE (416) 595-1155
TELEFAKE (416) 595-1163
TELEFAKE (416) 595-1163
TENDORMATION FOR SEQ ID NO: 7.
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100.0%; Pred. No. 1.9e-185;
tive 0; Mismatches 0;
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 715; Conservative
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Patent No. 5993169
GENERAL INFORMATION Michel H
APPLICANT: KLEIN, Michel H
APPLICANT: EWASYSHYN, MALY B
TITLE OF INVENTION: MILTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMBRIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF ESQUENCES: 38
NOTHERSPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                   9
                                                                                                                                           ACTACAAAACAACGCCAAAACAAACCACCAAAACAAACCCAATAATGATTTTTCACTTCGAA
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                                                      Gaps
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                       Length 920;
                   Query Match 100.0%; Score 715; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.9e-185;
Matches 715; Conservative 0; Mismatches 0;
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US-08-838-189D-7
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326 ATTACATCACAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 385
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14-NOV-1994
CLASSIEPTANTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iB: Sim & McBurney
330 University Avenue, 6th Floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 424
PRIOR APPLICATION A74:
APPLICATION NUMBER: GB 9200117.1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6033668
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MEDIUM TYPE: Floppy
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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M5G 1R7
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                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ENGINE HA
APPLICANT: DU RUN-Pan
APPLICANT: DU RUN-Pan
APPLICANT: DU RUN-PAN
TITLE OF INVENTION: CHINERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: 0'-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: 0'-MAY-1997
PILING DATE: 0'-MAY-1997
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION NUMBER: US 9200117.1
FILING DATE: 06-JAN-1992
ATFORNEY/AGENT INPORMATION:
NAME: STEWART, MICHAEA! I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Sim & McBurney
6th Floor, 330 University Avenue
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 715; Conservative
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ZIP: M5G 1R7
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COUNTRY: Canada
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421 ACCTTCAAGACAACCAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
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APPLICANT: Klein, Michel H
APPLICANT: Every Michel H
APPLICANT: Busy Shyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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US-08-467-969A-7
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-185;
Matches 715; Conservative 0; Mismatches 0; Indels
                                       NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
RESPERNCE DOCKET NUMBER: 1038-391 MIS
TELEPHONE: (416) 595-1153
TELEPHONE: (416) 595-1163
TELEPAX: 045-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: mucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-639E-7
FILING DATE: 06-JAN-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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385 445 241 ACTACAAAACAACGCCAAAACAAACAAACAAACACAATAATGATTTTCACTTCGAA 206 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGCAGATCAAGAACACA 121 ATTACATCACAAACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 326 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 181 CAACCCACAACAGTCAAGACTAAAAACACAACAACCAAACCCAAACCCAGCAAGCCA 446 ACTACAAACAACGCCAAAACAACCACCAAACAAACCAATAATGATTTTCACTTCGAA 1 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAGCCAGATCAAGAACACA ö Length 920; Indels COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
COMPOTHER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHER: BATENITIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIPICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIPICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIPICATION NUMBER: US 08/20117.1
FILING DATE: 06-JAN-1992
CLASSIPICATION NUMBER: 24-973
REPERENTION NUMBER: 24-973
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: 24-973
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: 24-973
FILING DATE: (416) 595-1165
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TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163 100.0%; Score 715; DB 3; L 100.0%; Pred. No. 1.9e-185; tive 0; Mismatches 0; APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Bwasyshyn, Mary E
TITLE OP INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
STREET: 330 University Avenue, 6th Floor Sequence 7, Application US/08467969A Patent No. 6168786 GENERAL INFORMATION: TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) LENGTH: 920 base pairs TYPE: nucleic acid STRANDEDNESS: single ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Florm:
COMPUTER: 715; Conservative Similarity STATE: Ontario US-08-467-969A-7 Query Match Best Local S: Matches 715 Š

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                       506 GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGGTATCTGC 565
                                                                                                                                                                                                                                    541 CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC 600
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GIGITIPACITIGIACCCIGCAGCATAIGCAGCAACAATCCAACCIGCTGGGCTATCIGC 360
                                                                         421 ACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Toronto
STATE: Ontario
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DEALING PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 24,973
REPERRORS/DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEPAX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
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330 University Avenue, 6TH Floor
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APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewayshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPLICATION UNMER: US/08/467,961A
PRILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION UNMERR: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRILING DATE: 06-JAN-1992
CLASSIFICATION: 435
PRILING DATE: 06-JAN-1992
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Patent No. 6171783
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                                  LENGTH: 920 base pairs
rTPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: DNA (genomic)
US-08-467-961A-7
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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46 CIGCICACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC 805
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APPLICANT: ENGASTHIN, Mury E
APPLICANT: BWASTHIN, Mury E
ATITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBULNEY
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                                                                601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
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                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.3%; Score 696; DB 2; L. Best Local Similarity 100.0%; Pred. No. 2.8e-180; Matches 696; Conservative 0; Mismatches 0;
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-ADR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            US-08-467-963C-28
; Sequence 28, Application US/08467963C
Patent No. 5968776
; GENERAL INFORMATION:
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
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COUNTRY: Canada
ZIP: M5G 1R7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-467-963C-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTACAAAACAACGCCAAAACAAACCACCAAACAACCAAATAATGATTTTCACTTCGAA 300
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                                                                                  STREET: 330 University Avenue, 6th Floor CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 715; Conservative
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STRANDEDNESS: single
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                                                             Ontario
: Canada
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RESULT 10
US-08-852-344D-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08838189D
Patent No. 2598169
Patent No. 2598169
Patent No. 2598169

APPLICANT: MICHAL H
APPLICANT: WIM.PERNATION: WULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: MULTIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: SIM & MCBULTHY
STREET: 6th Floor, 330 University Avenue
121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 180
                       379 CAACCCACAACAGTCAAGACTAAAACACAACAACAACCAAACACAACCCAGGAAGCCC 438
                                                                                                                                          241 ACTACAAAACAACGCCAAAACAAACCACCAAACAAACCAATAATGATTTTCACTTCGAA 300
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CITY: Toronto
STATE: Ontario
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC.TDGS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
TYING DATE: 16-APR-1997
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APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
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US-08-838-189D-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 ATTACATCACAAACCCCCCCATACTACCTTCAACAACCCAGGAGTCAAGTCAAACCTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CAACCCACACAGTCAAGACTAAAAACACAAACAACCAAAACAACCCAGCAAGCCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 cacaaagtcacacraacaacrocaarcaracaagarocaacaagacagarcagaacaca 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
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100.0%; Pred. No. 2.8e-180;
tive 0; Mismatches 0;
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                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 1038-687 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPROME: (416) 595-1155
TELEPRAT: (416) 595-1163
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                       APPLICATION NUMBER: GB 9200117.1 FILING DATE: 06-JAN-1992 ATTORNEY/AGENT INFORMATION: NAME: STEWART, MICHAEL I REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 696; Conservative
PRIOR APPLICATION DATA:
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499 GIGITTAACTTTGTACCCIGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTGC 558
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                                                                                                                                                                                                                                                                        619 ACCTICAAGACAACCAAAAAAGAICICAAACCICAAACCACIAAACCAAAGGAAGIACCC
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APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILNG DATE: 14-NOV-1994
CLASSIFICATION: 424
FRICK APPLICATION NUMBER: US 08/001,554
FILNG DATE: 06-JAN-1993
CLASSIFICATION: 424
FRICK APPLICATION 1424
FRICK APPLICATION 1424
FRICK APPLICATION 1424
FRICK APPLICATION WHERE: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 TCACAACCCTCATCTCCACCCAACACACACGCCAG 696
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330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038-391 MIS
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Patent No. 6033668
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEX: (65-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 28:
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ZIP: M5G 1R7
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STREET: 33
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 ATTACATCACAAACCACCACCACCATACTTCAACAACACCCAGGAGTCAAAGTCAAACCTG 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ACTACAAAACAACGCCAAAACAAACCAAACAAACAAATGATGATTTTCACTTCGAA 300
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Patent No. 6017539
GENERAL INFORMATION:
APPLICANT: MACHEN, Michel H.
APPLICANT: DU, Run-Pan
APPLICANT: BASYSHTN, Mary B
APPLICANT: MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHEN, MACHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,344D

FILING DATE: 07-MAY-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/344,639

FILING DATE: 14-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9200117.1

FILING DATE: 14-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: STEWNAT, Michael I

REGISTRATION NUMBER: 1038-688 MIS:jb

TELECOMUNICATION NUMBER: 1038-688 MIS:jb
                                                                                                                                                                                                                                                                                   STREET: Sim & MCBurney
STREET: 6th Ploor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
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                                                                                                                                   199 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACAACAA 258
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                                                                                                                                                                                      121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 180
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Patent No. 5998602
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Cirino, Nick M.
APPLICANT: Li, Guiying
APPLICANT: Xiao, Wei
TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES EFFECTIVE TO TREAT RSV INFECTIONS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                       CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACA
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                                                                            Length 894;
                                                                                                 Indels
                                                                       Query Match 97.3%; Score 696; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 2.8e-180;
Matches 696; Conservative 0; Mismatches 0;
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LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
JOPOLOGY: linear
US-08-344-639E-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-801-898A-23
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                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IDSKETTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASESO Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,898A
FILLING DATE: 18-FEB-1997
CLASSIFICATION: 514
ATTONNEY,AGENT INCRMATION:
NAME: POISBART BY BY ALCONNEY
REFRERENCE/DOCKET NUMBER: 28,462
REFRENCE/DOCKET NUMBER: 28,462
REFRENCE/DOCKET NUMBER: 8656-009
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEG-9741
TELECOMMUNICATION FOR SEG-9741
TELECOMMUNICATION FOR SEG-100-0005
INFORMATION FOR SEG ID NO: 23:
SEGURNICE CHARACTERISTICS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15222 base pairs
TYPE: nucleic acid
                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KEY: RSV-A2 | LOCATION: 1...15222 | CTHER INFORMATION: US-08-801-898A-23
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                                                                                                U.S.A.
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                                                                                                COUNTRY:
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Sequence 1, Application US/08892403A

Sequence 1, Application US/08892403A

Patent No. 5993824

GENERAL INFORMATION:

APPLICANT: Whitehead, Stephen S.

APPLICANT: Whitehead, Stephen S.

APPLICANT: Whitehead, Stephen S.

APPLICANT: Thinsz, Katalin

TITLE OF INVENTION: PRODUCTION OF ATTENUATED RESPIRATORY

TITLE OF INVENTION: SYNCYTIAL VIRUS VACCINES FROM CLONED NUCLEOTIDE SEQUENCES

NUMBER OF SEQUENCES: 14
  3857 ACCACCAAGCCCACGAAGAGCCAACCATCAACACCACCAAAACAACATCATAACTACA
                                                                     421 ACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                                                                  9797 CTACTCACCTCCAACACCACAGAAATCCAGAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                            9737 TCAACTTCCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTCTACAACATCCGAGTACCCA
                                                                                                                                                        601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,403A
FLING DATE: 15-JUL-1997
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US 60/047,634
FILING DATE: 23-MAY-1997
PRIOR APPLICATION NUMBER: US 60/046,141
PTING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 60/021,773
FILING DATE: 15-JUL-1996
ATTONNEY/AGENT INPORMATION:
NAME: PARMEDIA: 31,990
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 17634-000510 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
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nucleic acid
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COMPUTER READABLE FORM:
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5486 TCAACTTCCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTCTACAACATCCGAGTACCCA 5545
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Sequence 12, Application US/08962690

Patent No. 6214805

GENERAL INFORMATION:

APPLICANT: Torrence, Paul F.

APPLICANT: Cirino, Nick M.

APPLICANT: Cirino, Nick M.

APPLICANT: Li, Guiying

APPLICANT: Kiao, Wei

APPLICANT: Kiao, Wei

TITLE OF INVENTION: EFFECTIVE TO TREAT RSV INFECTIONS

FILE REFERENCE: 8656-019

CURRENT APPLICATION NUMBER: US/08/962,690

CURRENT FILING DATE: 1997-11-03

EARLIER APPLICATION NUMBER: 06/81,896

EARLIER APPLICATION NUMBER: 60/011,725

BARLIER APPLICATION NUMBER: 60/011,725

BARLIER APPLICATION NUMBER: 60/011,725

SEQIID NO.S: 40

SOFTWARE: Patentin Ver. 2.0

SEGID NO.S: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: respiratory syncytial virus US-08-962-690-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.8
Matches 677; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08720132
Patent No. 6264957
GENERAL INFORMATION:
APPLICANT: Collins, Peter L.
TITLE OF INVENTION: SYNCYTIAL VIRUS FROM CLONED NUCLEOTIDE SEQUENCES NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                        Gaps
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                                                            Score 654.8; DB 2; Length
Pred. No. 1.5e-168;
0; Mismatches 37; Indels
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                                                           91.6%;
                                                         Query Match
Best Local Similarity 94.8
Matches 677; Conservative
STRANDEDNESS: single
             TOPOLOGY: linear MOLECULE TYPE: CDNA
  ; STRANDEDNE;
; TOPOLOGY;
; MOLECULE TYPI
US-08-892-403A-1
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US-08-720-132-1
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,132
FILING DATE: 27-SEP-1996
CALSASTPICATION ADATA:
PRICATION NUMBER: US 60/007,083
FILING DATE: 27-SEP-1995
FILING DATE: 27-SEP-1995
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Pred. No. 1.5e-168;
0; Mismatches 37;
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 94.8
Matches 677; Conservative
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Search completed: October 30, 2003, 01:17:38 Job time : 57.5382 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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October 29, 2003, 16:50:52; Search time 244.018 Seconds (without alignments) 7909.644 Million cell updates/sec OM nucleic - nucleic search, using sw model US-09-462-816-3 715 IDENTITY NUC Scoring table: Perfect score: Seguence: Run on:

Total number of hits satisfying chosen parameters: 2552756 segs, 1349719017 residues Searched:

Gapop 10.0 , Gapext 1.0

5105512

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

| SIDSI/gcgdata/geneseq_embl/Nal990.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence encoding HRSV glycoprotein HSRV glycoprotein Polynucleotide seq Human respiratory Respiratory syncit Membrane bound G p Description AAQ45686 AAX08421 AAN70784 AAV18736 AAQ29623 AAX59703 AAX08422 Query Match Length DB 935 935 15210 15222 0.00 0.001

Score

М В Result

659 657.4 654.8 654.8

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| AAT63430 AAN17553 AAA68743 AAA68743 AAA28145 AAA7552 AAA88744 AAA25220 AAA718275 AAX35268 AAV18275 AAX352914 AAX352914 AAX352913 AAX352913 AAX35267 AAV18279 AAV18279 AAV18279 AAV18279 AAV18279 AAV18279 AAV18279 AAV18279 AAV18279 AAV18279 AAX35270 AAX35270 AAX35270 AAX35270 AAX35270 AAX35270 AAX35270 AAX35270 AAX35270 | |
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ALIGNMENTS

AAX08422 standard; cDNA; 715 28-JUN-1999 (first entry) AAX08422; RESULT 1 AAX08422

BP.

G protein gene fragment of respiratory syncytial virus.

G protein; respiratory syncytial virus; RSV; recombinant vector; vaccine; immune response; immunogenicity; tPA; antibody; tissue plasminogen activator; ss.

Respiratory syncytial virus (RSV).

1..702 /*tag= a /product= "Secreted G protein" Location/Qualifiers Key

WO9904010-A1

28-JAN-1999

protein gene fra

98WO-CA00697. 16-JUL-1998; 97US-0896442. 18-JUL-1997;

(CONN-) CONNAUGHT LAB LTD

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Claim 11; Figure 7A-7D; 80pp; English.
                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                         Respiratory syncitial virus
                                                                                                              AAQ45686 standard; DNA; 920
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(first entry)
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P-PSDB; AAR39286.
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13-JAN-1994
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                                                   Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and
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                                                                                                                                                                                                                                                                                                            100.0%; Score 715; DB 20;
100.0%; Pred. No. 1.4e-162;
tive 0; Mismatches 0;
                                                                                     raise antibodies for diagnosis
                                                                                                          Claim 8; Figure 3; 67pp; English.
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Best Local Similarity 100.
Matches 715, Conservative
                    WPI; 1999-132254/11
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                                              consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus (RSV)). The gene sequences that are particularly used are those which encode PIV-3 F and HIN proteins (AAQ45683, AAQ45684) and RSV F a G proteins (AAQ45684) and RSV F a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine; ss.
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/product= glycoprotein_G
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16..912
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86WO-US02756.
92US-0897171.
97US-0854783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-1986;
23-DEC-1986;
11-JUN-1992;
12-MAY-1997;
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          601 TCAACCICCTCCGAAGCAAICIAAGCCCTICICAAGICICCAAACAICCGAGCACCCA 660
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                           806 TCAACCICCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACAACATCGAGGACCA
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                                                                                    Sequence encoding human respiratory syncytial virus (HRSV) A2 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                  A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV sectines. The vactine can be administered to pregnant women or to women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines for human respiratory virus - comprising proteins or fragment encoded by a DNA sequence coding for human respiratory syncytial virus proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 92.2%; Score 659; DB 8; Length 935; al Similarity 95.1%; Pred. No. 4.5e-149; 680; Conservative 0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                            Human respiratory syncytial virus (HRSV).
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                                                                                                                                                                   AAN70784 Btandard; cDNA; 935
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(first entry)
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P-PSDB; AAP70845.
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Best Local Similarity
Matches 680; Conserv
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05-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                        Production of human respiratory syncytial virus glyco-protein F or (
- by culturing eukaryotic host cells transfected with corresponding
DNA.
                                                                                                                                                                                                                                                                                           The present sequence was used in the development of a novel method for the production of human respiratory syncytical virus (HRSV) glycoprotein G (GpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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92.2%; Score 659; DB 19; Length 935;
Best Local Similarity 95.1%; Pred. No. 4.5e-149;
Matches 680; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 935 BP; 383 A; 293 C; 100 G; 159 T; 0 other;
                                                                                                                                                                                                                                     Example 1; Columns 27-28; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines against HRSV.
                               WPI; 1998-144802/13.
P-PSDB; AAW47605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences of mRNA encoding HRSV structural proteins are given in AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                    Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K; major capsid protein; N; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prime the reverse transcription reaction for making the first strand of the CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes
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/note= "oligonucleotide used to specifically
/note= "oligonucleotide used to specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccines for human respiratory virus - include structural ge coding for native structural viral proteins and immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "oligonucleotide used to probe for
full length cDNA"
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                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus strain A2.
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                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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AAQ29623 standard; DNA; 935 BP.
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Disclosure; Fig 1; 98pp; English.
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                      CAACCCACAAAGACTAAAAAACACAAAAAACAACAACCCAAACACAACCCAGCAAGCCC
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                                                                               GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGCTATCTGC
                                                                                                                                                                                                                                                      New composition useful for inhibiting or treating infections against negative-strand RNA virus
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The specification describes a composition comprising a polynucleotide consisting of an antisense oligonucleotide containing a hydroxy group, complementary to the genomic or antisenonic strand of a negative-strand RNA virus, and an activator of RNAse L. The polynucleotide is used to inhibit, or treat, infection by negative-strand RNA viruses, specifically respiratory syncytial virus (RSV) but also (para)influenza, mumps, and rables. The polynucleotide can cross cell membranes without requiring carriers or permeabilizing agents, and can selectively cleave the RNA targeted by the oligonucleotide. The present sequence represents the polynucleotide sequence of RSV strain A2.
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91.6%; Score 654.8; DB 20
Best Local Similarity 94.8%; Pred. No. 9.4e-148;
Matches 677; Conservative 0; Mismatches 37;
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A human respiratory syncytial virus (RSV) anti-genome sequence (AAT63430) is the 5' to 3' positive-sense sequence of RSV; the genomitself is negative-sense. It was synthesised in segments by RT-FCR using intracellular RSV mRNA or genomic rRNA isolated from purified viruses as template. Restriction site markers were intoduced by incorporating the changes into the primers used for RT-FCR. The recombinant sequence can be expressed with a nucleocapsid protein, a large polymerase protein and an RNA elongation factor to produce isolated infectious RSV particles useful for generating vaccines against RSV. Recombinant RSV genome or also be used as a vector for gene therapy of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTACAAAACAACGCCAAAACCACCACCAAACAAACCCAATAATGATTTTCACTTCGAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence was used in the preparation of a novel polymucleotide, comprising an antisense oligonucleotide, with a polymucleotide, comprising an antisense oligonucleotide, with a polymucleotide arone end, that is complementary to 15-20 bases of the driving arone end of a respiratory syncytial virus (RSV), a linker attached to the OH-end of the antisense oligonucleotide and of a respiratory syncytial virus (RSV), a linker attached to the OH-end of the antisense oligonucleotide and polymucleotide can be transported across the call membranes without carriers or permeability agents, and once introduced destroys antisense target RNA. It also inhibits RSV infection in vitro in a superior manner to the conventional drug, ribavirin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymucleotide containing sequence anti-sense to region of RSV -
connected via a linker to an activator of RNaseL, used to treat RSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels
                                                                                                                                  Antisense oligonucleotide, respiratory syncytial virus;
RSV; treatment; infection; inhibition; strain A2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.6%; Score 654.8; DB 18; 94.8%; Pred. No. 9.4e-148; ive 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Torrence PF,
                                                                                        Human respiratory syncytial virus strain A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Pages 47-51; 89pp; English
                                                                                                                                                                                                      Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cirino NM, Li G, Silverman RH,
                                                                                                                                                                                                                                                                                                                                                                                                                            (CLEV-) CLEVELAND CLINIC FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US NAT INST OF HEALTH.
                                                                                                                                                                                                                                                                                                                                        97WO-US02531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-424748/39.
                                                                                                                                                                                                                                                                                                                                    14-FEB-1997;
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                                              17-MAR-1998
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5365 5425 5485 5545 099 480 900 5486 TCAACTICCTCCGAAGGCAATCCAAGCCTTCTCAAGTCTCTACAACATCCGAGTACCCA 5186 GIGITCAACITIGIACCCIGCAGCATAIGCAGCAACAATCCAACCTGCTGGGCTAICTGC 361 AAAAGAATACCAAACAAAAAACCAGGAAAGAAAACCACCACCAAGCCTACAAAAAAACCA 5246 AAAAGAATACCAAAAAAAACCAGGAAAAACCACTACCAAGCCACAAAAAAACCA 421 ACCTICAAGACAACCAAAAAAGAICTCAAAACCTCAAACCAAAACCAAAAGGAAGTACCC 5306 ACCCICAAGACAACCAAAAAAGAICCCAAACCICAAACCACIAAAICAAAGGAAGIAACCC 541 CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAAATGGAAACCTTCCAC 601 TCAACCICCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCCAACATCCGAGCACCCA Infectious respiratory syncytial virus particles - useful for treatment of RSV or gene therapy of upper respiratory tract diseases RSV; vaccine; gene therapy; upper respiratory tract disease; ss. Human respiratory syncytial virus strain A2 Respiratory syncytial virus anti-genome. (USSH) US DEPT HEALTH & HUMAN SERVICES Claim 46; Page 43-51; 66pp; English. BP.

Teng MN

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97WO-US12269.

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This is the 5'-3' positive sequence nucleotide sequence of respiratory syncytial virus (RSV) D46. The genome is negative-sense; the complete nucleotide sequence of the negative-sense; the complete nucleotide sequence of the wild-type B-1 virus has also been determined (see AAV1752).

A novel infectious recombinant RSV comprises a RSV genome or antigenome, a major nucleocapsid (N) protein, a nucleocapsid polymerase elongation factor, where the recombinant RSV has at polymerase elongation factor, where the recombinant RSV has at temperature-sensitive (Es) substitution at amino acid Phe521, along two attenuating mutations, one of the mutations specifying a temperature-sensitive (Es) substitution at amino acid Phe521, along two attenuating mutations, one of the mutations and phe521, along the substitution in the gene-start sequence of gene or a ts nucleotide substitution in the gene-start sequence of gene or a ts nucleotide substitution in the gene-start sequence of gene or a comprises a recombinant RSV paintijele which a RNA polymerase elongation factor, where the (anti)genome is modified:

(i) to ablate or modulate expression of a SH, NSI, NS2 or Gene or a cis-acting regulatory sequence; and (ii) by a termination codon introduced within a selected gene, or by a change in sequence, position or presence of a GS or GE transcription signal relative to the selected gene, or by a change in sequence, position or presence of a GS or GE transcription signal relative to the selected gene, (2) an expression vector; and (3) an RSV strain selected gene, or by a change in sequence or a selected gene, or by a change in sequence or a transcription and a capacited from CDES (ATCC WR 2453), cpts 248/404 (ATCC WR 2451), cpts 248/4009 (ATCC WR 2451), cpts 248/4009 (ATCC WR 2451) or cpts 530/1030 (ATCC WR 2452), or cpts 530/1030 (ATCC WR 2452), or cpts 530/1030 (ATCC WR 2452), or correspond a similar the immune system of a mindividual to induce in a vaccine to similar by a mindividual to induce a similar by a mindividual to induce a 
                                                                                                                                                                                                                                                           Attenuated respiratory syncytial virus vaccines - useful to protect
individuals against RSV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the production of infectious attenuated RSV particles.
                                                                                                                                                                 Collins PL, Juhasz K, Murphy BR,
                                                                                                                                                                                                                                                                                                                 Example 7; Page 188-195; 238pp; English
                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                   97US-0047634.
96US-0021773.
97US-0046141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protection against RSV
                                                                                                                                                                                                                      WPI; 1998-110579/10.
                                                                                                                                                                 Bukreyev AA,
Whitehead SS;
                   15-JUL-1997;
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                 Sequence 15223 BP; 5921 A; 2704 C; 2361 G; 4236 T; 1 other;
                                                                                          Indels
                                                   Query Match 91.64; Score 654.8; DB 18; Best Local Similarity 94.84; Pred. No. 9.4e-148; Matches 677; Conservative 0; Mismatches 37;
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5006 5126 0; 5007 ATTACATCACAAAATCACCACCATACTAGCTTCAACAACAACAGGGGTCAAGTCAAGTCAACCCTG 5066 180 240 4887 CACAPAGTCACACCAACAACTGCAATCATACAAGATGCAACAAGACACA 4947 Accelarcarectereda anterica de trada de la recentra del recentra de la recentra de la recentra della de 121 ATTACATCACAAACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 61 ACCCCAACATACCTCACTCAGGATCCTCAGCTTGGAATCAGCTTCTCCAATCTGTAAA 1 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGGCAGATCAAGAACACA Gaps Score 654.8; DB 19; Length 15223; Pred. No. 9.4e-148; 0; Mismatches 37; Indels 0; (Query Match 91.6%; Best Local Similarity 94.8%; Matches 677; Conservative 셤 쉽 Š ò 셤 ò 셤 ઠે

RSV; attenuation; vaccine; pneumonia; bronchiolitis; ss.

Human respiratory syncytial virus D46

409802530-A1

22-JAN-1998

Respiratory syncytial virus antigenome

(first entry)

20-JUL-1998

AAV17553

AAV17553 standard; cDNA; 15223 BP

(2) is used for

The expression vector of

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5486
                                                  5187 GTGTTCAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGGCTATCTGC 5246
                                                                                                                                                           5247 AAAAGAATACCAAACAAAAAACCAGGAAAGAAAACCACTACCAAGGCCCACAAAAAAACCA 5306
                                                                                                                                                                                                                                                    5487 TCAACTTCCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTCTACAACATCCGAGTACCA 5546
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GIGITITAACITITGIACCCIGCAGCAIAIGCACCAACAAICCAACCIGCIGGGCIAICIGC 360
                                                                                                                                                                                                                      ACCTTCAAGACAACCAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC 480
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                                                                                                         AAAAGAATACCAAAAAAAACAAGGAAAGAAAAACCACCACCAAGCCTACAAAAAAACCA
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/note= "creates SphI site in F/M2 intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= f
/note= "creates Stul site in G/F intergenic region"
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/note= "creates StuI site in G/F intergenic region"
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in the NS2-N intergenic region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Human respiratory syncytial virus. Chimeric - Bacteriophage T7.
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                                                                                                                                                                                                                                                                                           Infectious chimeric respiratory syncytial virus (RSV) produced from cloned nucleotide sequences, useful as a vaccine against diseases caused by the virus, such as pneumonia and bronchiolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to achieve protection against multiple RSV strains and/or subgroups
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15223 BP; 5921 A; 2705 C; 2361 G; 4236 T; 0 other;
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                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                    Example 7; Page 262-268; 280pp; English.
                                                                                                                                                                                                  Murphy BR, Whitehead SS;
                                               31-MAR-2000; 2000WO-US08802.
                                                                                              13-APR-1999; 99US-0291894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric nucleic acid construct for immunizing animals and humans against respiratory syncytial virus (RSV), comprises a sequence adapted for expression in plants and a RSV protein or peptide coding sequence
ACCCTCAAGACAACCAAAAAAGATCCCAAACCTCAAACCACTAAATCAAAGGAAGTACCC
                               ACCTTCAAGACAACQAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
                                                                       ACCACCAAGCCCACAGAAGAGCCCAACCATCAACACCCCAAAACAACATCATAACTACA
                                                                                                               CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                   TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCAACATCCGAGCACCCA
                                                                                                                                                                           TCAACTICCTCCGAAGGCAATCCAAGCCCTTCTCAAGTCTTTACAACATCCGAGTACCCA
                                                                                                                                                                                                           TCACAACCTTCATCTCCACCCCAACACACGCCAGTAGTTACTTAAAAACATA 5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a chimeric nucleic acid construct comprising: a nucleotide sequence adapted for protein expression in plants; and a respiratory syncytial virus (RSV) coding sequence encoding an RSV protein or an antigenic protein or peptide of RSV. The construct can be used to immunize animals and humans against respiratory syncytial virus. The use of transgenic plants to generate the antigen allows the production of greater amounts of
                                                                                                                                                                                                Chimeric; respiratory syncytial virus; RSV; immunize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krasnyanski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 10; 67pp; English.
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                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                 Human RSV G-protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korban SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-122707/13
                                                                                                                                                                                                                                                                      AAC88494 standard;
                                                                                                                                                                                                                                                                                                                                                                                              WO200068392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                          CACAAAGTCACACCAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACA
                                                                                                                                                                                                    CAATCCACAAAACGCCAAAAAACACAAAAAACCCAAAAAACCCCAAGCAAGCCC
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                                                              ACCITICAAGACAACCAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
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protein"

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Gaps

Score 649.6; DB 22; Length 918; Pred. No. 8.1e-147; 0; Mismatches 34; Indels 0;

Query Match
Best Local Similarity 95.2%;
Matches 670; Conservative

Sequence 918 BP; 366 A; 293 C; 100 G; 159 T; 0 other;

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exogenous nuclear acid encoding a paramyxovinus (PWN) protein or its antigenic fragment. The virus may be administered in combination with an antigenic fragment. The virus may be administered in combination with an antiviral tementherapeutic compound. Two or more viruses corpositions of the comprising different PWN proteins nay be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PWN in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous nucleic acid encoding a second pWN protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PWN protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral vector encoding a PWN protein. The recombinant virus is useful as an effective vaccine against hPV or RSV (the major causes of paediatric interest in target calls, providing a positive medical impact on interest in target calls, providing a positive medical impact on into stem cells effects a cure for sickle cell disease or beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACATCACAAAATCACCACCATACTAGCTTCAACAACACCAGGAGTCAAGTCAAGTCAACCCTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 ACCACAAAACAACGCCAAAACAAACCACCAAGCAAAACCAATAATGATTTTTCACTTTGAA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACAAAGTCACCAACAACTGCAATCATACAAGATGCAACAAGCCAGATCAAGAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ACTACAAAACAACGCCAAAACAAACCACCAAAACAAACCAATAATGATTTTCACTTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACCCACACAGTCAAGACTAAAACACAACAACAACCCAAACACAAACGCGGCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thalassaemia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The Sendai virus replicate at level that is high enough to induce sufficient immunity, but does not cause any harm to human recipient. The present sequence encodes a respiratory syncytial virus (RSV) G protein (heavily glycosylated protein), a PMV protein suitable for expression by the recombinant virus of the invention.
                                                                                                                                                                                                                                                                                                                                                                            Recombinant Sendai virus useful in vaccines to protect infection by paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant Sendai virus comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

90.4%; Score 646.2; DB 24; Length 897;
Best Local Similarity 95.3%; Pred. No. 5.3e-146;
Matches 666; Conservative 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 897 BP; 359 A; 289 C; 95 G; 154 T; 0 other;
                                                                                                                                                                                                   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 47; 57pp; English.
                                                                                               22-MAY-2001; 2001WO-US16610.
                                                                                                                                                 01-JUN-2000; 2000US-208701P.
                                                                                                                                                                                                                                                Portner A, Takimoto T;
                                                                                                                                                                                                                                                                                                  WPI; 2002-130534/17.
                                                                                                                                                                                                                                                                                                                             P-PSDB; AAU74676.
WO200192548-A2.
                                               06-DEC-2001
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301 GIGTTTAACTTTGTACCCTGCAGCATATGCAACAACCAACCTGCTGGGCTATCTGC 360
                                                                                                                        420
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                                                                                                                                                                                                                                                                                                                                                                            739 CTACTCACCTCCAACACCACAGGAAATCCAGAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA
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                                                                                                                                                                                                                                                421 ACCTICAAGACAACCAAAAAGAICTCAAACCICAAACCACTAAACCAAAGGAAGIACCC
                                                                                                                                                                                                                                                                                                         619 ACCCTCAAGACAACCAAAAAGATCCCAAACCTCAAACCACTAAATCAAAGGAAGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 CTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid containing pneumococcal epitope for expression in eukaryotic cells - useful for eliciting immunological response to pneumococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSV; glycoprotein G; pneumococcal surface protein A; PspA;
infection; Streptococcus pneumoniae; sepsis; otitis media;
meningitis; bacteraemia; pneumonia; vaccine; genetic immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory syncytial virus glycoprotein G gene portion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 TCACAACCCTCATCTCCACCCAACACACACGCCAGTAG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           859 TCACAACCTTCATCTCCCACCAACACACACACCACCAGTAG 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Curiel DT, McDaniel LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1C; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV38298 standard; DNA; 696 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US22847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0759505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYAL-) UNIV ALABAMA.
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WO9802530-A1

22-JAN-1998

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membrane where it can be exposed to the host immune system.

Insertion of pneumococcal surface protein A (PBpA) coding sequence created plasmid pKSD2601. Intramuscular immunisation of BALBA/C mice with pKSD2601 induced protection against an otherwise lethal cohallenge with a capsular type 3 pneumococcus. A claimed plasmid for expression of pneumococcal epitope DNA in extravoric cells includes a promoter for driving expression in a eukaryotic cells includes a promoter for driving expression in a eukaryotic cells (e.g. HCMV-IE), DNA encoding a leader sequence (e.g. of RSVG) can DNA encoding a pneumonoccal epitope such as PspA. The invention also provides a vaccine comprising the plasmid and a suitable carrier or diluent, and optionally one or more cytokines or DNA encoding them, or a bacterial delivery system. The vaccine is used to elicit an immunological response in a host, including humans, susceptible to pneumococcal infection or sepsis. The plasmid can also be used to express a pneumococcal epitope of interest in vitro.
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258
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                                                     CATTCCACAACAGTCAAGACCAAAAACACAACAACAAACTCAAACTCAAACACAACCCAGGAAGCC
                                                                                                                                                                                                                      1 CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAGCCAGATCAAGAACACA
                                                                                121 ATTACATCACAAACCACCACCATACTAGCTTCAACAACACCGGGGGGTCAAGTCAAACCTG
                                                                                                                                                                 CAACCCACAACAGTCAAGACTAAAAACACAAAC-AACCCAAACACCAACCAGCAAGCC
                                                                                                                                                                                                         AGTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACAATCCAACCTGCTGGGCTATCTG
                                                                                                                                                                                                                                                                      AGTGTTCAACTTTGTACCCTGCAGCATATGCAGCAACAACCTGCTGGGGCTATCTG
                                                                                                                                                                                                                                                                                           CAAAAGAATACCAAACAAAAACCAGGAAAGAAAACCACCACCAAGCCTACAAAAAAACC
                                                                                                                                                                                                                                                                                                                                   420 AACCTTCAAGACAACCAAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACC
                     1; Gaps
DB 19; Length 696;
Score 445.8; DB 19; Length
Pred. No. 8.4e-98;
0; Mismatches 22; Indels
Query Match
Best Local Similarity 95.3%;
Matches 470; Conservative
                                                                                                                                                                                                                                                                                                                                                                           CACCACCAAGCCC 492
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5008 ACCACATCACCAATCCACACAATTCAGCCACAACATCACCCAACACAAAGTCAGAAACA 5067
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A novel infectious recombinant RSV comprises a RSV genome or antigenome, a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a large polymerase protein (L), and a RNA polymerase elongation factor, where the recombinant RSV has at least two attenuating mutations, one of the mutations specifying a temperature-sensitive (ES) substitution at amino acid Rhe521, and the RSV polymerase gene or a ts nucleotide substitution in the gene-start sequence of gene MZ. Comprises a recombinant RSV (anti)genome, N, P, and L proteins, RNA polymerase elongation factor, where the (anti)genome is modified. (i) to ablate or modulate expression of a SH, NS1, NS2 or G gene or introduced within a selected gene, or by a change in sequence, position or presence of a GS or GB transcription signal relative to the selected gene; (2) an expression vector; and (3) an RSV strain selected from cpts RSV 248 (ATCC WR 2450), opts 248/404 (ATCC WR 2452). Cpts 830/1009 (ATCC WR 2451) or cpts 530/1009 (ATCC WR 2452) or E-1 cp52/285 (ATCC WR 2451) or cpts 530/1009 (ATCC WR 2452) or estimate recombinant RSV and RSV particles are used in a vaccine attenuated recombinant RSV and RSV particles are used in a vaccine of estimation of estimated recombinant RSV and RSV particles are used in a vaccine of estimation of estimated attenuated recombinant RSV and RSV particles are used in a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CACAAAGICACTAACAACIGCAAICATACAAGAIGCAACAAGCCAGAICAAGAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ACCCCAACATACCTCACTCAGGATCCTCAGCTTGGAATCAGCTTCTCCAATCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4948 Arcaccarcracciracricandreceacasasases rascereredas acertaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ATTACATCACAAACCACCATCATAGCTTCAACAACACCAGGAGTCAAGTCAAACCTG
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                                                                                                                                                                                                                                                                                                                                                                         Attenuated respiratory syncytial virus vaccines - useful to protect individuals against RSV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.0%; Score 300.4; DB 19; Length 15225; 64.6%; Pred. No. 1.8e-62;
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                                                                                                                                                                                                                                                                    Teng MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to stimulate the immune system of an individual to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 251; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protection against RSV. The expression vector of (2) the production of infectious attenuated RSV particles.
                                                                                                                                                                                                                                                                  Juhasz K, Murphy BR,
                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 195-202; 238pp; English
                                                                                      97WO-US12269.
                                                                                                                             97US-0047634
                                                                                                                                                                           97US-0046141
                                                                                                                                                    96US-0021773
                                                                                                                                                                                                                                                                Collins PL,
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                                                                                                                                                                                                                                                                                                                                  WPI; 1998-110579/10.
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                                                                                                                                                                                                                                                                Bukreyev AA,
Whitehead SS;
                                                                                    15-JUL-1997;
                                                                                                                                23-MAY-1997;
                                                                                                                                                                           09-MAY-1997;
                                                                                                                                                  .5-JUL-1996;
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RSV; attenuation; vaccine; pneumonia; bronchiolitis; ss.

syncytial virus genome.

(first entry)

20-JUL-1998

AAV17552;

AAV17552 standard; cDNA; 15225 BP

Human respiratory syncytial virus B-1

241 ACTACAAAACAACGCCAAAACAAACCACCAAAACAAACCAAATAATGATTTTTCACTTCGAA 300

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5128 AGCACAAAACCACGTAAAAAATCCACCAAAAAAACCAAAAAAGTGATTACCATTTTGAA 5187
                                                                   5248 AAAACAATACCAAGCAACAAACCAAAGAAACCAACCATCAAACCAAAACAAAACCA 5307
                                                                                                   ACCTICAAG----ACAACCAAAAAGATCICAAACCICAAACCACTAAACCAAAGGAAGTA 477
                                                                                                                   538 ACACTGCTCACCAACAACACCACAGGAAATCCAAAACTCACAAGTCAAATGGAAACCTTC 597
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Search completed: October 29, 2003, 22:09:35 Job time: 246.018 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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| cleic - nucleic search, using sw model | 1: October 29, 2003, 16:51:32 ; Search time 2923,85 Seconds (without alignments) 10004.074 Million cell updates/sec | : t score: 715 1cacaaagtcacactaacaacgtagttattaaaaaaaaa 715 | ng table: IDENTITY_NUC Gapop 10-0 , Gapext 1.0 | led: 2888711 segs, 20454813386 residues | number of hits satisfying chosen parameters: 5777422 | um DB seq length: 0 um DB seq length: 2000000000 | orocessing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | GenEmbl:* 1: 9D ba:* 3: 9D hg:* 4: 9D on:* 5: 9D ov:* 7: 9D ph:* 9: 9D ph:* 10: 9D ph:* 11: 9D ph:* 12: 9D ph:* 13: 9D ph:* 14: 9D ph:* 15: em_Da:* 16: em_Lin:* 18: em_lin:* 18: em_lin:* 18: em_lin:* 22: em_ov:* 23: em_pat:* 24: em_ph:* 25: em_ov:* 25: em_ov:* 26: em_vo:* 27: em_pat:* 28: em_lin:* 29: em_vi:* 29: em_vi:* 21: em_ph:* 22: em_ov:* 23: em_pat:* 24: em_ph:* 25: em_tin:* 26: em_vi:* 27: em_tig_lin:* 28: em_htg_lin:* 31: em_htg_lin:* 32: em_htg_lin:* 33: em_htg_lin:* 34: em_htg_lin:* 35: em_htg_lin:* 36: em_htg_lin:* 37: em_htg_lin:* 36: em_htg_lin:* 37: em_htg_lin:* 36: em_htg_lin:* 37: em_htg_lin:* 36: em_htg_lin:* 37: em_htg_lin:* |
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| Regult No. S | Score | Query Match | Length | DB | ID | |
| ! | 715 | 188 | 715 | ٠ | 18 | 34 Nucleic |
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| | 969 | | 894 | | AR080424 | |
| 14 | 6 96 8 8 | 97.3 | 894 | 9 7 | AR092548 beulce | AR092548 Sequence |
| 16 | 54.8 | | 15222 | | AR093219 | AR093219 Sequence |
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| | 8. 4.0 | | 15222 | 4 4 | HRU50362 HRU50363 | US0362 Human respi |
| | 24.8 | | 15222 | - | HRU63644 | U63644 Human respi |
| | 8. 6 | | 15222 | 4 | RSHSEQ | M74568 Human respi |
| | 6.4.0 | | 15223 | ٥ ٢ | AF035137 | AR089137 Sequence AR035006 Himan res |
| | 9.6 | | 914 | 4 | PARSENVG | X03149 Respiratory |
| | 9.6 | | 918 | | AX047075 | AX047075 Sequence |
| | 11.8 | | 15190 | ₹# | HRU39662 | MASSBOLL Sequence U39662 Himan respi |
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| | 20.8 | | 887 | 4 4 | AKS VGL12 AF065409 | สลา |
| | 20.5 | | 918 | 14 | AF065405 | Human |
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| | 18.7 | | 9 2 2 2 2 2 | 4 4 | HKSUGGLY2 | Z33454 Human respi |
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| BD081934 LOCUS DEFINITION | BD08 | BD081934 Nucleic acid | id vaccines | ines | 715 bp DNA encoding G protein of | linear PAT 27-AUG-2002 respiratory syncytial |
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| KEYWORDS SOURCE ORGANISM | JP 7 Resp | JP 20015126 Respiratory Respiratory | JP 2001512662-A/2. Respiratory syncytial Respiratory syncytial | tial | virus vimis | |
| avisagaaa | Viru | ses; | skna ne ridae; | gati | and viruses; nae; Pneumovi | Mononegavirales; .rus. |
| AUTHORS | Li,X | K., Sam | Sambhara, S. and | 15) S. an | d Klein, M.H. | |
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/mol_type="genomic DNA"
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Sequence 7 from patent US 5968776.
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AR080406.1 GI:10007141
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
95 c 290 g 380 t
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Synthetic RSV G gene (seq ID No: 7).
A16258
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Location/Qualifiers
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synthetic construct
artificial sequences.
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Klein, W.H., Du, R.-E. and Bwasyshyn, M.E.
Multimeric hybrid gene encoding a chimeric protein which confers
protection against parainfluenza virus and respiratory syncytial
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481 ACCACCAAGCCCACAGAAGAGCCAACCATCAACACCACCAAAACAACATCACAACTACA
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100.0%; Score 715; DB 6; Length 920;
Best Local Similarity 100.0%; Pred. No. 3.3e-151;
Matches 715; Conservative 0; Mismatches 0; Indels (
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| | Query Match 100.0%; Score 715; DB 6; Length 920; Best Local Similarity 100.0%; Pred. No. 3.3e-151, 0; Gaps 0; Atches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CACAAAGTCACATACAACAACAGCAATCATACAAGAACAACAACAACAACAACAACAACAACAACAACAA |
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| 421 ACCTTCAAGACAACCAAAAAGATCTCAAACCACTAAACCAAAGAAGAAGTACCC 480 | Query Match 100.0%; Score 715; DB 6; Length 920; Best Local Similarity 100.0%; Pred. No. 3.38-15; Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CACAAACTCACATAACAACTCAATCATACAAGACAACAACACAACACAACACAACACAACACACAACA |

| Db 566 AAAGAATACCAAAGAAACCAGGAAAGAAAACCACCACCACCACCAAAAAA | | 541 746 | | | RESULT 8 AR148357 LOCUS LOCUS LOCUS DEFINITION Sequence 7 from patent US 6225091. VERSION AR148357 VERSION KEYWORDS COURCE SOURCE CORGANISM UNKNOWN. | | JOURNAL Patent: US 6225091-A 7 01-MAY-2001; FEATURES Location/Qualifiers 1920 | /organisme="univ | Query Match 100.0%; Score 715; DB 6; Length 920; Best Local Similarity 100.0%; Pred. No. 3.3e-151; Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps | . 206 206 | 266 | | | QY 241 ACTACAAAACACGCCAAAACCACCAAAACCAACAAACCAATAATGATTTTCACTTCGAA 300 Db 446 ACTACAAAACCAACACCAAAACCAACCAACCAAAACCAACCAATAAT | Ay 301 GTGTTTBACTTTGFACCCTGCAGATATGCAGCAATCCAACCTGCTGGGCTATCTGC 360 |
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| | DD 626 ACCTTCAAGACAACAAAGATCTCAAACCTCAAACCATAAAGGAAGTACCC 685 QY | | OY 601 TCAACCTCCTCCGAAGGCAATCTAAGCCCTTCTCAAGTCTCCACAACATCCGAGCACCCA 660 | Qy 661 TCACAAACCCTCATCTCCACACAACAACAGGGGGGGGTAGTTATAAAAAAAA | RESULT 7 AR123540 920 bp DNA Linear PAT 16-MAY-2001 LOCUS BEFINITION Sequence 7 from patent US 6171783, ACCESSION AR123540 GI:14108901 KEYWORDS Niknown. ORGANISM Unknown. ORGANISM | Unclassified. Unclassified. AUTHORS Klein,M.H., Du,RP. and Ewasyshyn,M.E. TITLE Infection detection method using chimeric protein JOURNAL Patent: US 6171783-A 7 09-JAN-2001; FRATURES Location/Qualifiers | source 1. 920 // Arganism="unknown" // Arganism="unknown" 180 a 290 c 95 g 155 t | tch 100.0%; Score 715; DB 6; Length 920; 18 Similarity 100.0%; Pred, No. 3.3e-151; 15. | CACAAAGTCACACTAACAAC | 61 ACCCAACATACCTCACCAGGATCCTCAGGTTGGAATCAGCTTTCTCCAATCTGTCTG | ATTACATCACAAACCACCACCACCATCACACACACAACACAACA | CAACCCACAACAGTCAAGACTAAAAACAACAACAACAACCCAAACACAAACACAGACCGGGCCCCIG | 241 ACTACAAAACAACCCAAAACAAACCACCAAAACAAACAA | | Db 506 GTGTTTAACTTTGTACCCTGCAGCATATGCAGCAACCAAC |

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g protein.

Human respiratory syncytial virus

Human respiratory syncytial virus

Human respiratory syncytial virus

Human respiratory syncytial virus

Yiruses; ssRNA negative-strand viruses; Mononegavirales;

Paramyxoviridae; Pneumovirinae; Pneumovirus.

[ (bases 1 to 923)

Garcia-Barreno, B., Portela, A., Delgado, T., Lopez, J.A. and

Melero, J.A.

Frame shift mutations as a novel mechanism for the generation of

neutralization resistant mutants of human respiratory syncytial
                                                   326 ATTACATCACAAACCACCACATACTAGCTTCAACAACAACCAGGAGTCAAGTCAAACCTG
                                                                                                              506 GIGITTAACTITGTACCCTGCAGCATATGCAGCAACAATCCAACCTGGGCTATCTGC
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    .923
/organism="Human respiratory syncytial virus"

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/protein_id="CAA34937.1"
/db_xref="G1:60307"
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/db_xref="taxon:11250"
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Nucleic acid vaccines encoding G protein of respiratory syncytial
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PN JP 2001512662-A/1
PD 28-AUG-2001
PP 16-JUL-1998 JP 2000503216
PR 18-JUL-1997 US 08/896442
PI XIAOMAO LI,SURYAPRAKESH SAMBHARA,MICHEL H KLEIN PC C12N15/09,A61K48/00,C07K16/10,C12P21/08,C12Q1/68,G01N33/53, PC C12N15/00
CC Nucleic acid vaccines encoding G protein of respiratory C
                                ACCTTCAAGACAACCAAAAAAGATCTCAAAACCTCAAACCCACTAAACCAAAGGAAGTACCC
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              361 AAAAGAATACCAAACAAAAACCAGGAAAGAAAACCACCACCCAAGCCTACAAAAAACCA
                                                                          421 ACCTTCAAGACAACCAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
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/mol type="genomic DNA"
/db_xref="taxon:12814"
290 c 95 g 155 t
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JP 2001512662-A/1.
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/db_xref="SPTREMBL:001929"
/translation="MSKNKDQRTAKTLEKTWDTLAYLLPISSGLYKLNLKSIAQITLS
ILAMISTISLIITALIPASANHKYTLTTAIIQDATSQITWTPTYLTYDDDLGISPS
NLSEITSQTTILASTTPGVKSNLQPTYKTKOMTTTTQTQPSKPTTKQRQNKPDRKPN
NDFHFBVFRVPVCSICSNNPTCWAICKRIPHKTAKTGKTKTTKTTKTTKPTKKPTKKTTKKDLKPP
TTKPRKBVPTTKPTEEPTINTTKTNITTTLLINNTTGNPKLTSQMETFHSTSSEGNLSP
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100.0%; Pred. No. 4.4e-150;
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HRSVGL16 922 bp RNA linear VRL 05-JUN-1997
Human respiratory syncytial virus (MON-7-91) subgroup A, G gene for g1ycoprotein.
233429.
G gene; G1:485888
G gene; Glycoprotein.
Human respiratory syncytial virus
Human respiratory syncytial virus

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

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Dopazo,J.
Dipacec Submission
Birect Submitsed (10-MAY-1994) Dopazo J., Centro Nacional de Biotecnologia
- CSIC, Biolnformatica, Universidad Autonoma, Cantoblanco, Madrid, SPAIN, 28049
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Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.

1 (bases 1 to 922)
Sarcia,O., Martin,M., Dopazo,J., Arbiza,J., Fabrasile,S., Hortal,M., Perez-Brena,P., Martinez,I., Garcia-Barreno,B.
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/organism="human respiratory syncytial virus"
/mol_type="genomic RNA"
/strain="aubgroup A"
/isolate="MON 7 91 (Montevideo/Uruguay, 1991)"
/db_xref="taxon:11250"
/coll line="HEp-2"
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/db_xref="G1:333941"

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Location/Qualifiers
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                                                                                                             634 ACCTICAAGACAACCAAAAAGATCTCAAACCTCAAACCACTAAACCAAAGGAAGTACCC
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attachment glycoprotein; surface glycoprotein.
Human respiratory syncytial virus
Human respiratory syncytial virus
Wituses; serNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.

E 1 (bases 1 to 917)
S Johnson, P.R., Spriggs, M.K., Olmsted, R.A. and Collins, P.L.
The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between antigenically related proteins
E Proc. Natl. Acad. Sci. U.S.A. 84 (16), 5625-5629 (1987)
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/organism="Human respiratory syncytial virus"
//Ob_xref="taxon:11250"
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Pred. No. 1.2e-147;
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Best Local Similarity 99.6%;
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Klein,M.H., Du,R.-P. and Ewasyshyn,M.E.
Multimeric hybrid gene encoding a chimeric
protection against parainfluenza virus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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Sequence 28 from patent US 5968776.
AR080424. GI:10007159
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Location/Qualifiers
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/organism="unknown"
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RSHICE
Human respiratory syncytial virus nonstructural protein (1C),
nonstructural protein (1B), major nucleocapsid (N), protein (1C),
(P), protein (M), 1A (1A), G (G), protein (F) and
envelope-associated protein (22K) gene, complete cds.
MI1486 K01459 K02719 K03348 K03349 MI1217 MI1244 MI1487 MI1505
MI1514 MI1631 MI2966
MI156.1 GI:333225
envelope-associated protein; fusion glycoprotein; major
nucleocapsid protein; major surface glycoprotein; matrix protein;
nonstructural protein; phosphoprotein.
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0; Gaps
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Nucleic Acids Res. 11 (17), 5941-5951 (1983)
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
1 (bases 165 to 2220; 5254 to 5544)
Elango,N. and Venkatesan,S.
0; Indels
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  CACAAAGTCACACTAACAACTGCAATCATACAAGATGCAACAAGAGCAGATCAAGAACACA 60
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Klein, M.H., Du, R.-P. and Ewasyshyn, M.E.
Multimeric hybrid gene encoding a chimeric protein which confers
protection against parainfluenza virus and respiratory syncytial
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Sequence 28 from patent US 5998169.
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Satake,M., Elango,N. and Venkatesan,S.
Sequence analysis of the respiratory syncytial virus phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                             Collins, P.L. and Wertz, G.W.
The envelope-associated 22K protein of human respiratory syncytial
virus: nucleotide sequence of the mRNA and a related polytranscript
J. Virol. 54 (1), 65-71 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (bases 8 to 1050; 7554 to 8506)
Blango,N., Satake,M. and Venkatesan,S.
mRNA sequence of three respiratory syncytial virus genes encoding
two nonstructural proteins and a 22K structural protein
J. Virol. 55 (1), 101-110 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 (bases 4630 to 5543)
Satake, M., Coligan, J.B., Blango, N., Norrby, E. and Venkatesan, S.
Respiratory syncytial virus envelope glycoprotein (G) has a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of the G protein gene of human respiratory syncytial virus reveals an unusual type of viral membrane protein Proc. Natl. Acad. Sci. U.S.A. 82 (12), 4075-4079 (1985)
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Collins, P.L. and Wertz, G.W.
Nucleotide sequences of the 1B and 1C nonstructural protein mRNAs of human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Respiratory syncytial virus fusion glycoprotein: nucleotide sequence of mRNA, identification of cleavage activation site and amino acid sequence of N-terminus of F1 subunit Nucleic Acids Res. 13 (5), 1559-1574 (1985)
                                                      Satake, M. and Venkatesan, S.
Nucleotide sequence of the gene encoding respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 (bases 4627 to 5544)
Martz,G.W., Collins,P.L., Huang,Y., Gruber,C., Levine,S. and
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nucleotide sequence of the mRNA and a related polycistronic
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Elango,N., Satake,M., Coligan,J.E., Norrby,E., Camargo,E.
Venkatesan,S.
                                                                                                                                                                                                                                                                                                 4 (bases 5602 to 7500)
Collins, P.L., Huang, Y.T. and Wertz, G.W.
Nucleotide sequence of the gene encoding the fusion (F)
glycoprotein of human respiratory syncytial virus
Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7683-7687 (1984)
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                                                                                                                                                                                                                                             Virol. 52 (3), 991-994 (1984)
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                                                                                          virus matrix protein
J. Virol. 50 (1), 92-99 (1984)
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Collins, P.L. and Wertz, G.W.
The 1A protein gene of humar
                                      (bases 3211 to 4157)
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13 (bases 1051 to 1080, 2278 to 2287, 3192 to 3210, 4158 to 4172, 4572 to 4626; 5545 to 5601, 7501 to 7578)
Collins, P.L., Dickens, L.E., Buckler-White, A., Olmsted, R.A., Spriggs, M.K., Camargo, E. and Coelingh, K.V.
Nucleotide sequences for the gene junctions of human respiratory syncytial virus reveal distinctive features of intergenic structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reprint for [2] and clean copy sequence for [12], [5] kindly provided by P.Collins, 21-FEB-1986.
Respiratory syncytial virus is a negative-strand RNA pleomorphic enveloped virus of the genus Pneumovirus. The matrix protein has no homology with the matrix proteins of other negative-stranded RNA viruses, implying that RS virus has undergone extensive evolutionary divergence. Two unidentified reading frames which potentially encode proteins were located: one overlaps the matrix protein and the other the P protein. The biological significance of these two reading frames is not clear. The positive strand is
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LECIGIKPTKHTPIIYKYDLNP"
12 (bases 1081 to 2277)
Collins.P.L., Anderson,K., Langer,S.J. and Wertz,G.W.
Correct sequence for the major nucleocapsid protein mRNA
respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4594-4598 (1986)
86259643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Human respiratory syncytial virus"
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                                                                                                                                     Virology 146 (1), 69-77 (1985)
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1: Sp_archea:*

2: Sp_bacteria:*

3: Sp_fungi:*

5: Sp_human:*

6: Sp_mranal:*

7: Sp_mranal:*

8: Sp_phage:*

7: Sp_phage:*

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8: Sp_virus:*

4: 15: 16: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

| Description | Q82068 human respi | Q01929 human respi | 009719 respiratory | 009634 human respi | Q9q6t8 human respi | Oggeuo human respi | Q9yvb5 human respi | Q82066 human respi | Q9yvb3 human respi | Q9yvb4 human respi | Q82071 human respi | Q9q6t3 human respi | Q9yvb2 human respi | human | _ | Q82067 human respi | |
|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--|
| qı | Q82068 | Q01929 | 009719 | 009634 | Q9Q6T8 | 019060 | Q9YVB5 | 982066 | Q9YVB3 | Q9YVB4 | 082071 | Q9Q6T3 | Q9YVB2 | 082058 | 086359 | Q82067 | |
| DB | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | |
| Query Match Length DB | 298 | 298 | 298 | 298 | 279 | 279 | 297 | 297 | 293 | 298 | 297 | 278 | 292 | 297 | 295 | 297 | |
| Query | 100.0 | 100.0 | 88.9 | 88.9 | 88.5 | 87.2 | 86.8 | 86.7 | 86.5 | 86.4 | 85.9 | 85.8 | 85.7 | 85.7 | 85.6 | 85.2 | |
| Score | 1229 | 1229 | 1093 | 1093 | 1088 | 1072 | 1067 | 1066 | 1063 | 1062 | 1056 | 1055 | 1053 | 1053 | 1052 | 1047 | |
| Result No. | Н | 7 | ო | 4 | S | 9 | 7 | 89 | O | 10 | 11 | 12 | 13 | 14 | 15 | 16 | |

| O91947 human respi | Q9q6t1 human respi | respir | Q9q6s0 human respi | human | human | human | Q9q6ul human respi | human | human | human | human | human | respir | | human | human | human | human | | Q86357 respiratory | Q9q6s1 human respi | human | human | human | human | human | human | Q82062 human respi |
|--------------------|--------------------|--------|--------------------|--------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|--------|--------|--------|--------|--------|--------------------|
| 091947 | Q9Q6T1 | 096360 | 089060 | Q9Q6R9 | Q9YVB1 | Q82065 | Q9Q6U1 | 082074 | Q82064 | Q9Q6S2 | Q9YVB0 | 689060 | 086361 | 082063 | Q9Q6T4 | 989060 | Q9Q6T9 | Q82077 | Q9Q6S7 | 086357 | 090681 | Q9YVC8 | 091946 | 082060 | 982072 | 082079 | Q82057 | Q820 <i>6</i> 2 |
| 7 12 | • • | • • | • | • | • | • | • | | • | • | • | • • | • | ٠. | ٠. | • | • | | 9 12 | ٠. | • | • | ٠. | • | • | | • | ω |
| 29 | 27 | 29 | 27 | 27 | 5 | 29 | 27 | 29 | 29 | 27 | 29 | | | | | 27 | 27 | 29 | 279 | | | | 53 | 29 | 53 | 29 | 29 | 29 |
| 85.2 | 85.0 | 85.0 | 84.9 | 84.9 | 84.9 | 84.9 | 84.7 | 84.6 | 84.6 | 84.5 | 84.5 | 84.4 | 84.4 | 84.4 | 84.3 | 84.3 | 84.2 | 84.2 | 84.1 | 84.1 | | 84.0 | 84.0 | 83.9 | 83.7 | 83.6 | 83.6 | 83.6 |
| 1047 | 1045 | 1045 | 1044 | 1044 | 1044 | 1043 | 1041 | 1040 | 1040 | 1039 | 1039 | 1037 | 1037 | 1037 | 1036 | 1036 | 1035 | 1035 | 1033 | 1033 | 1032 | 1032 | 1032 | 1031 | 1029 | 1028 | 1028 | 1028 |
| 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | | 40 | 41 | 42 | | 44 | 45 |

ALIGNMENTS

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STRAINS BUDGING A.

K. MEDLINE-94335057; PubMed-8057427;
MEDLINE-94335057; PubMed-8057427;
MEDLINE-94335057; PubMed-8057427;
Medicia O., Martin M., Dopazo J., Fabrasile S., Russi J.,
A. Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
Melero J.A.;
Melero J.A.;

"Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic C. Anages in the G glycoprotein.";
J. Virol. 68:5448-5459 (1994).

R. EMBL; Z33429; CAA83872.1;
ILLE-PRO; IPRO00925; Glycoprot G.
InterPro; IPRO00625; Glycoprot G.
InterPro; IPRO0062; Glycoprotein G.; I.
R. Pfam; PF00802; Glycoprotein G.; I.
R. Pfam; PRO0012; PHOSPHOPAÑTETHEINE; 1.
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Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 232; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                  Human respiratory syncytial virus.
Viruses; sRRN megative-strand viruses; Mononegavirales;
Paramyxoviridae; Pheumovirinae; Pheumovirus.
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                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
dlycoprotein (Fragment).
                                     PRT; 298 AA.
                                   PRELIMINARY;
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127 QPTTVKTKNYTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALC 186
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                      127 QPTTVKTKONTTTTQTQPSKPTTKQRQNKPPNKPNNFHPEVFNFVPCSICSNNPTCWALC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91065351; PubMed=2249671; Garcia-Barreno B., Portela A., Delgado T., Lopez J.A., Melero J.A.; Garcia-Barreno B., Portela A., Delgado T., Lopez J.A., Melero J.A.; Rrame shift mutations as a novel mechanism for the generation of newtralization resistant mutants of human respiratory syncytial
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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InterPro; IPR000925; Glycoprot G.
InterPro; IPR006162; Ppantne aftach.
Pfam, PPG0802; Glycoprotein G; 1.
PROSITE; PSG0012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 298 AA; 32771 MW; F8CD4213D97C2952 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                              "Identification of mutations contributing to the reduced virulence of a modified strain of respiratory syncytial virus.", V_{accine 14:1637-1646 (1996)}.
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                                                                    STRAIN=S2 t81C;
SIRDLINE=S7185152; PubMed=9032893;
Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A., Ionghurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J.,
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            Baston A.J.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000925; Glycoprot G.
InterPro; IPR06162; Ppantne attach.
Pfam, PF00802; Glycoprotein G; I.
BROSTIR; P800012; PHOSPHOPANTETHENE; 1.
SEQUENCE 298 AA; 32779 MW; 67F4A043682FA450 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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MEDLINE=97185152; PubMed=9032893;
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Matches 209; Conservative
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                  NCBI_TaxID=12814;
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Choi B.H., Lee H.J.;

"Generic diversity and molecular epidemiology of the G protein of

subgroups A and B of respiratory syncytial virus isolated over 9

consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556 (2000).
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                                                                                             88.9%; Score 1093; DB 12; Length 298; 90.1%; Pred. No. 1.9e-78; ive 6; Mismatches 17; Indels 0;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
           InterPro; IPR000925; Glycoprot_G.
InterPro; IPR006162; Ppattne attach.
Pfam; PF00802; Glycoprotein G; 1.
PROSTITE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 298 AA; 32749 MW; 60F27B29D4997F31 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycoprotein (Fragment).
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InterPro; IPR006162; Ppantne attach.
Pfam; PF00802; Glycoprotein G; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
NON TER 1 1
SEQÜENCE 279 AA; 30499 MM; 4EICDF2F71
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Best Local Similarity 90.1%;
Matches 209; Conservative
EMBL; U39662; AAC57026.1; -.
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Best Local Similarity 90.19
Matches 209; Conservative
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Q9Q6T8
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48 HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSETTSQTTTLASTTPSVESTL 107
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                         228 LLINNITGNPEHTSQKETLHSTSSEGNPSPSQVYTTSRYLSQPPSPSNTTNQ 279
181 LLINNTIGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Human respiratory syncytial virus.
Viruses; sEMAn negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=99022964; PubMed=9806017;
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"Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";
J. Virol. 68:5448-5459(1994).

EMBL: Z33427; CAA83870.1;
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Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.,
"Antigenic and genetic diversity among the attachment proteins of
infortions and genetic diversity among the attachment proteins of
infoctions in children...,
J. Infect. Dis. 178:925-932(1998).
EMBL, AF065405; AAD02941...,
InterPro; IPR000925; Glycoprot. G.
InterPro; IPR000925; Glycoprot. G.
InterPro; IPR006162; Ppantine attach.
Fram; PF008012; PH0SPF0ENTETHEINE; I.
SEQUENCE 297 AA; 32572 MW; 5C10E719A05EF5C1 CRC64;
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MEDLINE=94335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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InterPro; IPR006162; Ppantne attach.
Pfam; PF00802; Glycoprotein G; PR05802; Glycoprotein G; PR0581TE; PS00012; PHOSPHOPAMTETHEINE; 1.
SEQUENCE 297 AA; 32589 MW; F210F8C68193F5DD CRC64;
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Last annotation update)
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88.7%; Pred. No. 2.1e-76;
ive 7; Mismatches 15
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Matches 205; Conservative
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Best Local Similarity
Matches 204; Conserv
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KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTBEPTINTTKTNITT 180
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Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
"Antigenic and genetic diversity among the attachment proteins of group A respiratory syncytial viruses that have caused repeat infections in children...;
J. Infect. Dis. 178:1925-932 (1998).
EMBL; AP065477; AAD02943.1:
InterPro; IPR006925; Glycoprot. G.
InterPro; IPR006165; Ppantne attach.
Fram, Pr008021; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                          247 LLTSNTTRNPELISQMETFHSTSSEGNPSPSQVSITSEYPSQPSPSNTSR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TYEMBLrel. 10, Created)
01-MAY-1999 (TYEMBLrel. 10, Last sequence update)
01-MAY-2003 (TYEMBLrel. 13, Last annotation update)
Attachment glycoprotedin G (Fragment)
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein G.
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WV6973;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus.
Viruses, ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID=11250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 AA; 30443 MW; 8E2974F2E1AE15C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=20283719; PubMed=10823752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                             E STRAIN=WT5222;

XX MEDLINE=99022964; PubMed=9806017;

XA SUllender W.W., Muteon M.A., Frince G., Anderson L.J., Wertz G.W.;

XA Sullender W.W., Muteon M.A., Frince G., Anderson L.J., Wertz G.W.;

XA Sullender W.W., Muteon M.P., Frince G., Anderson L.J., Wertz G.W.;

XI Tatigenic and genetic diversity among the attachment proteins of RT group A respiratory syncytial viruses that have caused repeat

XI Infections in children.";

XI Infect Dis. 178:922-1999.

XI Infect Dis. 178:922-11 - .

XI EMBL; AF065406; AAD02942.1; - .

XI INTERPOOF; PROMOSICE; PPANTING G.

XI INTERPOOF; PROSPHOPANTETHEINE; I.

XI PROSITE; PS00012; PHOSPHOPANTETHEINE; I.

XI SEQUENCE 298 AA; 32781 MW; ABTC9E05547C5745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Evolutionary pattern of human respiratory syncytial virus (subgroup A): cocirculating lineages and correlation of genetic and antigenic changes in the G glycoprotein.";

changes in the G glycoprotein.";

EMBL; 233432; CAA83875.1;

EMBL; 233422; CAA83875.1;

InterPro; IPR000925; Glycoprot G, InterPro; IPR000125; Pantne attach.

PEam; PF00802; Glycoprotein G; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=94335057; PubMed=8057427;
MEDLINE=94335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
Melero J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 LLINSTIGSPEHTSQKETLHSTSSEGNPSPSQVYTTSKYLSQPPSPSNITWQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LLTNNTTGNPKLTSOMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.4%; Score 1062; DB 12; Length 2 Best Local Similarity 87.5%; Pred. No. 5.2e-76; Matches 203; Conservative 9; Mismatches 20; Indels
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NCBI_TaxID=11250;
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67 HKVTSTTTIIODATNOIKNTTPTYLTONPOLGISPSNPSBITSLITTLLDSTTPGVKSTL 126
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"Genetic diversity and molecular epidemiology of the G protein of Subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556 (2000).

EMBL; AF193313; AAF23736.1;
InterPro; IPR000925; Glycoprot G.
InterPro; IPR000925; Glycoprot G.
InterPro; IPR000125; Ppantne attach.
Pfam; PP00802; Glycoprotein G; 1.
Prosyner: PROSYINE; PSO0012; PHOSPHOPANTETHEINE; 1.
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G protein (Fragment).
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Jurol. 68:548-5459(1994).
EMBL; Z33456; CAA83879.1; -.
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MEDLINE=94335057; PubMed=8057427;
Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
                                                                                                                                  Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
"Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
infections in children."

J. Infect. Dis. 178:925-932(1998).

BMID., APG65408; AAAD02944.1;
InterPro; IPR0006162; Ppantne attach.
InterPro; IPR000655; Glycoprot G.
InterPro; IPR000655; Prich extens.
Fram; PP00802; Glycoproted.
Fram; PP00802; Glycoproted.
Fram; PR00802; Glycoproted.
FRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; I.
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                                            Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VICBI_TaxID=11250;
                                                                                                                                                                                                                                                                                                     SEQUENCE 292 AA; 31964 MW; 8942A8DD0A402A4B CRC64;
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Attachment glycoprotein G (Fragment).
Human respiratory synoytial virus.
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                                                                                                                            MEDLINE=99022964; PubMed=9806017;
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Matches 203; Conservative
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MEDLINE-9134005; PubMed-1895054;
MEDLINE-9134005; PubMed-1895054;
MIDDLINE-9134005; PubMed-1895054;
MIDDLINE-9134005; PubMed-1895054;
MIDDLINE-9134000 Of Variable domains of the attachment (G) protein of subgroup A respiatory syncytial vuruses.";
J. Gen. Virol. 72:2091-2096(1991).
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                                                                                                                                85.7%; Score 1053; DB 12; Length 87.4%; Pred. No. 2.7e-75; live 8; Mismatches 21; Indels
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STRAIN=RSB99-6256;
Cane P.A.;
Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; X73353; CAA51764.1; -..
InterPro; IPR006925; Glycoprot G.
InterPro; IPR006162; Papattne affach.
Pfam; PP00812; Pypoprotein G; 1.
PROSITE; PS00012; PHOSPHOPANTETHBINE; 1.
InterPro; IPR006162; Ppantne attach. Pfam; PF00802; Glycoprotein \overline{G}_{i} 1. PROSITE; PS00012; PHOSPHOPANTETHEINE; 1. SEQUENCE 297 AA; 32741 MW; 0E567A174BF64964 CRC64;
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01-NOV-1996 (TrEMBirel. 01, Last seq
01-MAR-2003 (TrEMBirel. 23, Last ann
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201; Conservative
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185 KRIPNKKPGKKTTTKPTKKPTIKTTKKDLKPQTTKPKEVLTTKPTEKPTINTTRTNIRTT 244

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Search completed: October 29, 2003, 17:40:53 Job time : 55.717 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 29, 2003, 17:12:25 ; Search time 12.6943 Seconds Run on:

(without alignments) 859.454 Million cell updates/sec

US-09-462-816-4 Perfect score:

1 HKVTLTTAIIQDATSQIKNT.....VSTTSEHPSQPSSPPNTTRQ 232 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | P20895 human respi | 3 human | human | human | P27026 human respi | human | human | P27021 human respi | human | P20896 human respi | P02840 drosophila | | Q02817 homo sapien | | | | O10683 bovine resp | Ol0684 bovine resp | P22261 bovine resp | Ol0687 bovine resp | O10685 bovine resp | P08640 saccharomyc | | P57999 oryctolagus | Q28983 sus scrofa | P13728 drosophila | Q86695 ovine respi | Ol0686 bovine resp | 009495 bovine resp | Q84183 bovine resp | homo | O9hc84 homo sapien | rattr |
|----------------------------|--------------------|------------|------------|------------|--------------------|------------|-------|--------------------|------------|--------------------|-------------------|-------|--------------------|------------|------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|----------|
| ID | VGLG HRSVL | VGLG HRSVA | VGLG HRSV6 | VGLG HRSV3 | VGLG HRSV7 | VGLG HRSV4 | | VGLG HRSV2 | VGLG HRSV8 | VGLG HRSV1 | SGS3_DROME | | MUC2 HUMAN | MUC1 XENLA | SGS3_DROSI | DAN4 YEAST | VGLG BRSV1 | VGLG_BRSV4 | VGLG BRSVC | VGLG BRSVW | VGLG BRSV2 | AMYH YEAST | VGLG_BRSV7 | ZAN RABIT | ZAN PIG | SGS3 DROYA | VGLG ORSVW | VGLG BRSVS | VGLG BRSVL | VGLG BRSVR | MUSA HUMAN | MUSB HUMAN | MIC2 RAT |
| DB | -1 | - | ۲4 | н | Н | ч | ۲ | H | н | н | Н | ~ | Н | - | -1 | -1 | н | Н | Н | H | - | -1 | Н | Н | М | - | Н | ч | Н | Н | Н | Н | Н |
| % Query Match Length | 298 | 298 | 297 | 297 | 297 | 297 | 298 | 297 | 292 | 292 | 307 | 2812 | 5179 | 662 | 217 | 1161 | 263 | 263 | 257 | 263 | 263 | 1367 | 257 | 2282 | 2476 | 263 | 263 | 257 | 257 | 257 | 1233 | 5703 | 1513 |
| % Query Match | 98.9 | 91.1 | 85.6 | ĸ | 84.4 | | 82.9 | 82.1 | 41.1 | 40.4 | 16.4 | 16.2 | 15.7 | • | 14.9 | 14.9 | 14.7 | 14.6 | 14.4 | • | 13.9 | | | 13,5 | | • | 13.0 | ٠ | | • | 12.5 | 12.5 | 12.2 |
| Score | 1216 | 1120 | 1052 | 1045 | 1037 | 1033 | 1019 | 1009 | 505.5 | 497 | 202 | 198.5 | 193 | 191 | 183 | 183 | 180.5 | 179.5 | 177 | 176.5 | 170.5 | 169.5 | 169 | 166 | 164.5 | | 159.5 | 159 | 156 | 154 | 15 | 153.5 | 150.5 |
| Result No. | - | 8 | m | 4 | S) | 9 | 7 | B | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 |

| 1178 1 YS89 CAEEL 797 1 VGEA HAVEB 907 1 VGEA HAVEB 908 1 CHI2_COCPO 3376 1 ZAN MOUSE 1260 1 ALSI_CANAL 886 1 VGP3 EBYAB 1240 1 VGP3 EBYAB 1240 1 VGP3 EBYAB 1240 1 VGP3 EBYAB 1240 1 MUAL XEBLA 1251 AMYH SACDI 1267 1 P60 IJSIN 1271 VGP_MABVM 1271 VGP_MABVM | Q09624 caenorhabdi | P28968 equine herp | P03200 epstein-bar | P54197 coccidioide | 088799 mus musculu | P46590 candida alb | Q07284 epstein-bar | Q09550 caenorhabdi | P10667 xenopus lae | P04065 Baccharomyc | Q01836 listeria in | P35253 marburg vir |
|---|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 875000000774 | YS89_CAEEL | VGLX_HSVEB | VGP3 EBV | CHI2_COCPO | ZAN MOUSE | ALSI CANAL | VGP3_EBVA8 | YOU3 CAREL | MUA1 XENLA | AMYH SACDI | P60 LISIN | VGP_MABVM |
| | 8 | 7 | 7 | 0 | 6 1 | 0 | 1 | 10 | 0 | 7 1 | 7 1 | 1 |
| | 12.2 | 12.0 | 12.0 | 12.0 | 11.8 | 11.8 | 11.6 | 11.5 | 11.4 | 11.3 | 11.2 | 11.2 |
| 20000000000000000000000000000000000000 | | | 'n | 47 | 5.5 | 14.5 | 143 | 141 | 39.5 | 139 | 138 | 37.5 |
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenically related proteins.",
Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
-!- FUNCTION: VALIES PARAMYXOVIRUS ATTACHBENT PROTEINS, THE
PRESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURRACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- PTM: MAX CARRY 40-80 SEPRARTE OILINKED CARBOHYDRATE CIRINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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N-LINKED (GLCNAC. . ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.; The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between
                                                                                                                                                                                                                                  Human respiratory syncytial virus (subgroup A / strain Long).
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Pred. No. 4.3e-75;
0; Mismatches 2; Indels (
                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                                     Viruses; seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; 1PR000925; Glycoprot G. Pfam; PP00802; Glycoprotein G; 1. Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=87289657; Pubmed=2441388;
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Best Local Similarity 99.1
Matches 230; Conservative
   STANDARD:
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298 AA;
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VGLG HRSVL
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                                  SOUTH THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO
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-I- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

-I- SUBCELLILLAR LOCATION: EXPRESSED ON THE SURFACE OF THE INPECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRLONS.

-I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINB AND THREONINE RESIDUES.
                                                                                                                                                               PRT;
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                                                    67 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                           QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHPEVFNFVPCSICSNNPTCWAIC
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HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=85216636; PubMed=3858865;
Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;
"Nucleotide sequence of the G protein gene of human respiratory
syncytial virus reveals an unusual type of viral membrane protein.",
Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
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Satake M., Coligan J.E., Elango N., Norrby E., Venkatesan S.;
"Respiratory syncytial virus envelope glycoprotein (G) has a r
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Viruses; sBRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VGI_TaxID=11259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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Pred. No. 1.2e-68;
5; Mismatches 12; Indels
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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135 135 N-LINKED (GLCNAC. .) (PO
237 237 N-LINKED (GLCNAC. .) (PO
251 251 N-LINKED (GLCNAC. .) (PO
254 251 81 N-LINKED (GLCNAC. .) (PO
258 AA; 32586 MW; 993G3D2DD68BC634 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; 1.
Transmembrane; Glycoprotein.
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InterPro; IPR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                          EMBL; M11486; AAB59857.1; --
EMBL; X03149; CAA26928.1; --
EMBL; U50362; AAB8665.1; --
EMBL; U50363; AAB86675.1; --
EMBL; U63644; AAC55969.1; --
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P27025;
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SEQUENCE
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                                                                                                                                                                                                                                       QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHPEVFNFVPCSICSNNPTCWAIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91374005; PubMed=1895054;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

J. Gen. Virol. 72:2091-2096(1991).

-! FUNCTION. UNLIKE THE OFFHER PARAMYZOVIRUS ATTACHMENT PROTEINS, THE PRAGAGIOTINATING ACTIVITIES.

-! SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-! FTW. MAY CARRY 40-80 SEBRARE O-LINKED CARBOHYDRATE CHAINS

DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                             0; Gaps
                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                     247 LLTINITGNPEYTSQKETLHSTSPEGNPSPSQVYTTSEYPSQPPSPSNTT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1045; DB 1; Length 297; Pred. No. 1.3e-63;
                                                                                                                                      85.6%; Score 1052; DB 1; Length 297;
                                                                                                                                               Pred. No. 4.2e-64;
6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus (strain rsb1734).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                   .LINKED (GLCNAC. . .) (PC
6781756C38B64A80 CRC64;
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                                  EXTRACELLULAR (POTENTIAL)
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           CYTOPLASMIC (POTENTIAL).
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N-LINKED
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                                                                                                            32708 MW;
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Glycoprotein.
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                                                                                                                                               Local Similarity 87.4 hes 201; Conservative
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297 AA;
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Best Local Similarity
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P27022;
         DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
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                                                                                   67 HKITSTTIIQDATNQIKNTTPTYLTQNPQLGISPSNBSDITSLITTILDSTTPGVKSTL 126
                                                                                                                                                                                 127 QSTTVGTKNTTTTQAQPNKPTTKQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                                                                                                                                              121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 180
                                                                                                                                                                                                                                                                                                                187 KRIPNKKPGKRTTTKPTKKPTPKTTKKGPKPQTTKSKEAPTTKPTEEPTINTTKTNIITT 246
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                                                    1 HKVTLITAIIQDAISQIKNTIPTYLIQDPQLGISFSNLSBITSQITTILASTTPGVKSNL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLLA AND INCORPORATED IN THE MEMBRARD OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEPRARTS O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE=91374005; PubMed=1895054; Cane P.A., Matthews D.A., Pringle C.R.; Identification of variable domains of the attachment (G) protein of
     0; Gaps
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135 N-LINKED (GLCNAC. . .) (POTENTIAL).
237 N-LINKED (GLCNAC. . .) (POTENTIAL).
251 N-LINKED (GLCNAC. . .) (POTENTIAL).
294 N-LINKED (GLCNAC. . .) (POTENTIAL).
32670 MM; 56B384028E437ACD CRC64;
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Pred. No. 4.3e-63;
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  200; Conservative 10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus (strain rsb6614).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
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67 HKVTLTTAIIQDATSQIKNTTQTYLLQNTQLGISFSNLSETTSQPTTTPALTTPSAKSTP 126
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                                   187 KRIPNKKPGKKTTTKPTKKPTKTTKKDLKPQTTKPKGVLTTKPTEKPTINTTKTNIRTT 246
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Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
J. Gen. Virol. 72:2091-2096(1991).
-1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUG G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLOTINATING ACTIVITIES.
-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRONS.
-1- FTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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BATRACELIULAR (POTENTIAL).

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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                   181 LLTWNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                          247 LLTTNTTGNPEYTSQKETLHSTSPEGNPSPSQVYTTSEYPSGPPSPSNTT 296
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Pred. No. 8e-63;
Triches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus (strain rsb5857).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last semotation update)
01-AUG-1992 (Rel. 23, Last amotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
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32772 MW; 10488CCA475936BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                         PRT;
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ThrerPro. 1PR000925; Glycoprot G.
Pfam; PF00802; Glycoprotein G; I.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.1%;
86.5%;
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
103
135
237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11254;
                                                                                                                                                                                                                                                                                                                                      VGLG HRSV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
CARBOHYD
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CARBOHYD
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Best Local 8
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VGIG HRSV4

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VGLG_HRSV5 RESULT 7

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61 OPTIVKTKUTTITOTOPSKPTTKORONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 QSTTVKTKNTTTTQIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 KRIPSKKPGKKTTTKPTKKPTKTTKTTKKDHKPQTTKPKEAPSTKPTEKPTINITKPNIRTT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                                                                                                                                                         MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane Lification of variable domains of the attachment (G) protein of "Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LLTINNTTGNPKLTSOMETFHSTSSEGNLSPSOVSTTSEHPSOPSSPPNTTRQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 EXTRACELLULAR (POTENTIAL).
103 N-LINKED (GLCNAC. .) (FOTENTIAL).
135 N-LINKED (GLCNAC. ..) (POTENTIAL).
237 N-LINKED (GLCNAC. ..) (POTENTIAL).
250 N-LINKED (GLCNAC. ..) (POTENTIAL).
32769 MW; 4D74E854D34D7BBAS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- FTW, MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
PIR; JQ1207; JQ1207.
InterProf; JR900925; Glycoprot, G.
Pfam; PF00802; Glycoprotein.
G; 1.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.9%; Score 1019; DB 1; Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7e-62;
.hes 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human respiratory syncytial virus (strain rsb642).
Viruses; ssRNA negative strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI TaxID:e11225;
                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                         Human respiratory syncytial virus (strain rsb6190).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
 298 AA.
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tive 10; Mismatches
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PRT;
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Matches 197; Conservative
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 STANDARD;
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGLG HRSV2
P27021;
 VGLG HRSV5
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DOMAIN
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFKFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                      1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                            subgroup A respiratory syncytial viruees.",
J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDMEd=1697126; MEDLINE=90357765; PubMed=1697126; Sullender W.M., Anderson K., Wertz G.W.; "The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of sequence, expression from a recombinant vector, and evaluation as an immunogen against homologous and heterologous
                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                        MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of
                                                                                                                                    -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE WEMERANE OF THE VIRIONS.
-!- PTM: MAY CARRY 40-480 SEPARATE O-LINKED CARECHURARE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 PLISNTARNPELISOMETFHSTSSEGNPSPSQVSITSEYPPQPSSPPNTPR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LLTNNTTGNPKLTSOMETFHSTSSEGNLSPSOVSTTSEHPSOPSSPPNTTR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus (subgroup B / strain 8/60).
                                                                                                                                                                                                                                                                                                                                                              82.1%; Score 1009; DB 1; Length 297; 84.0%; Pred. No. 3.2e-61; ive 11; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NUG-1992 (Rel. 23, Last amnotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses, ssRNA negative-strand viruses, Mononegavirales,
Paramyxoviridae, Pneumovirinae, Pneumovirus.
NCBI_TaxID=11258,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91374595; PubMed=1895391;
Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.;
                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                     FC72A7F3A8EBF67C CRC64;
                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 AA.
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                                                                                                                                                                                                         InterPro, IPR000925, Glycoprot_G. Pfam; PF00802, Glycoprotein_G; I. Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                           67 297 EX
135 135 N-
144 144 N-
237 237 N-
297 AA; 32745 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subgroup virus challenge.";
Virology 178:195-203(1990).
                                                                                                                                                                                                                                                                                                                                                                                         Matches 194; Conservative
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                                                                                                                                                                                             PIR; JQ1204; JQ1204
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              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRSV8
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                                                                                                                                                                                                                                                                                                                                                                             Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 HYVTLTTVTVQTIKNHTGKNISTYLTQVPPERVNSSKQPTTTSPIHTNSATISPNTKSET 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 KTIPSNKPKKKPTIKPTNKPTTKTTNKRDPKTPAKMPKKBIITNPTKKPTLKTTERDTST 246
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"Genetic diversity of the attachment protein of subgroup B respiratory syncytial viruses.";
J. Virol. 65:5425-5434 (1991).
-1- FUNCTION: UNLIKE THE OTHER PARAMYKOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGIUTINATING ACTIVITIES.
-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRARD OF THE VIRONS.
-1- PTM: MAY CARRY 40-80 SEPRANTE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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Viruses; seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11251;
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Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
"The G glycoprotein of human respiratory syncytial viruses of
subgroups A and B: extensive sequence divergence between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 505.5; DB 1; Length 292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 SQSTVIDTITPKYTIQQQSLASTTSENTPSSTQIPTASE-PS-TSNP 291
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EXTRACELLULAR (POTENTIAL)
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01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AA
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InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 66 FO
67 292 EX
81 81 N-
86 86 N-
100 100 N-
292 AA; 32143 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M55633; AAA47413.1; -.
EMBL; M73545; AAA47408.1; -.
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les 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 OPTIVKTKNITITIQIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPQTTKPKEVPTTKPTBEPTINTTKTNITT 179
           Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
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Garfinkel M.D., Pruitt R.E., Meyerowitz E.M.;
"DNA sequences, gene regulation and modular protein evolution in the
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                      -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endoptera, Endoptera, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                         40.4%; Score 497; DB 1; Length 292; 46.8%; Pred. No. 6.9e-27; ative 28; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TLLINNTIGNPKLISOMETFHSISSEGNLSPSQVSTISEHPS 221
                                                                                                                                                                                                                                                                                      66 POTENTIAL.
292 EXTRACELLULAR (POTENTIAL).
81 N-LINKED (GLCNAC. .) (PC
86 N-LINKED (GLCNAC. .) (PC
100 N-LINKED (GLCNAC. .) (PC
32306 MW; BC8C59F69CA7AFCZ CRC64;
                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 SQSTVLDTITPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
6-CCT-2001 (Rel. 40, Last annotation update)
Salivary glue protein Sgs-3 precursor.
SGS3 OR CG11720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 307 AA
                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila 68C glue gene cluster.";
J. Mol. Biol. 168:765-789(1983).
                                                                                                                                                                                                                           PIR, B32703, MGNZ18.
InterPro. 1 PR00925, Glycoprot G.
Pfam, PF00802; Glycoprotein G: 1.
Transmembrane; Glycoprotein.
antigenically related proteins.";
                                                                                                                                                                                                                 EMBL; M17213; AAA47412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                292 AA;
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                                                                                                                                                                                                                                                                                                                            CARBOHYD
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93; Indels 48; Gaps 13;
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                                                                                                                                                                                62 PITVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICK 121
                                                                                                                                  4 TLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGV--KSNLQ 61
                                                                                                                                                         49 TTTTTTCAPPTQQ-STTQPPCTTSKP-----TTPKQTTTQLPCTTPTTKATTTK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
MEDLINE=99018118; PubMed=9799733;
Glockner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
Glockner G., Rosenthal A.;
"Large-scale sequencing of two regions in human chromosome 7q22:
analysis of 650 kb of genomic sequence around the BPO and CUTL1 loci
reveals 17 genes.";
Genome Res. 8:1060-1073 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller W., Koop B.F.; "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                 177 ITTILITNNTIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTR 231
                                                                                                                                                                                                                                                                                               Gao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21138439; PubMed=11239002;
Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
Cheung T.D., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  ZAN HUMAN STANDARD; PRT; 2812 AA.
Q9Y493; O00218; Q96L85; Q96L87; Q96L88; Q96L99; Q96L90;
Q9BXN9; Q9BZ83; Q9BZ84; Q9BZ86; Q9BZ87; Q9BZ88;
                                                                               / Match 16.4%; Score 202; DB 1; Length 307; Local Similarity 32.8%; Pred. No. 4.4e-07; les 77; Conservative 17; Mismatches 93; Indels 4
                                              SALIVARY GLUE PROTEIN SGS-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Testis;
Cheung T.L., Wassler M.J., Cornwall G.A., Hardy D.M.;
"Multiple intra-species variants of human zonadhesin.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                 1 23 POTENTIAL.
24 307 SALIVARY GLUE PROTEIN SGS-
307 AA, 32196 MW, 45803DED16C418BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).
                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2375-2683 FROM N.A. (ISOFORM 7).
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           FlyBase; FBgn0003373; Sgs3.
Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zonadhesin gene (ZAN).";
                                                                                                                                                                                                                                                                                                                                                                                                                                            Zonadhesin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
PIR; A03329; GSFF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                          SEQUENCE
                                                                                 Query Match
                                  SIGNAL
                                                                                                         Matches
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Genomics 41:119-122(1997).
-1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- DOWAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRAPTING OF THE WIGUN-LIKE DOWAIN MIGHT INHIBIT INAPPROPRIATE TRAPTING OF SPERMANOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.

-I- DOWAIN: The VWFD domain 2 may mediate covalent oligomerization (by similarity to human intestinal mucin MUC2).

-I- SIMILARITY: Contains 4 VWFD domains.

-I- SIMILARITY: Contains 4 VWFD domains.

-I- SIMILARITY: Contains 1 RGF-like dowain.

-I- SIMILARITY: Contains 1 RGF-like dowain.

-I- SIMILARITY: Contains 1 RGF-like dowain.

-I- SIMILARITY: Contains 1 RGF-like dowain.

-I- SIMILARITY: Contains 1 RGF-like dowain.
                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOId=Q9Y493-7; Sequence=VSP_001426, VSP_001427;
-!- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
-!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLICCIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016324; C:apical plasma membrane; NAS.
GO; GO:000333; P:binding of sperm to zona pellucida; NAS.
GO; GO:0008037; P:cell recognition; NAS.
GO; GO:0016337; P:cell recognition; NAS.
InterPro; IPR006209; RGF like.
InterPro; IPR002319; TIL Cysrich.
InterPro; IPR003328; TILā Cysrich.
InterPro; IPR003328; TILā Cysrich.
InterPro; IPR0030346; VWF C.
InterPro; IPR001346; VWF D.
PF00629; MAM; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1;
IsoId=Q9Y493-2; Sequence=VSP_001430, VSP_001431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=09Y493-4; Sequence=VSP_001424, VSP_001425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sold=Q9Y493-3; Sequence=VSP_001428, VSP_001429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBOId=Q9Y493-5; Sequence=VSP_001420, VSP_001421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [Bold=Q9Y493-6; Sequence=VSP_001422, VSP_001423;
                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                      -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9Y493-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY046055; AAL04414.1; -...
EMBL; AY046055; AAL04415.1; -...
EMBL; AF053356; AAC78790.1; ALT_SEQ.
EMBL; BA312032; AAK21011.1; -...
EMBL; U83191; AAC51208.1; -...
Genew; HGNC:12857; ZAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF332975, AAKO1431.1; --
EMBL, AF332977, AAKO1432.1; --
EMBL, AF332977, AAKO1433.1; --
EMBL, AF332977, AAKO1434.1; --
EMBL, AF332978, AAKO1435.1; --
EMBL, AF332980, AAKO1435.1; --
EMBL, ARVA6055, AALO4410.1; --
EMBL, AYO46055, AALO4411.1; --
EMBL, AYO46055, AALO4411.1; --
EMBL, AYO46055, AALO4412.1; --
EMBL, AYO46055, AALO4412.1; --
EMBL, AXO46055, AALO4413.1; --
EMBL, AXO46055, AALO4413.1; --
EMBL, AXO46055, AALO4413.1; --
                                                                                                                                                                                                                                                                                                -!- ALTERNATIVE PRODUCTS
                                                                                                                              SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                       Name=3;
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DR Pfam; PF01826; TIL; 4.

DR Pfam; PF02345; TILa; 5.

DR Pfam; PF00345; TILa; 5.

DR SWART; SW00181; EGF; 4.

DR SWART; SW00214; VWC; 4.

DR SWART; SW00216; VWC; 4.

DR SWART; SW00216; VWD; 4.

DR PROSITE; PS01086; EGF 1; 1.

DR PROSITE; PS01080; EGF 2; 4.

DR PROSITE; PS0060; MAM 2; 3.

W RSPEART; Alternative splicing.

W Repear; Alternative splicing.

T SIGNAL.

1 7 DENOMINE.
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AGOD (in 1soform ?).
/FTId=VSP_001427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGYSSRYHISELYDTLPSILCQPGRPRGLRGPLRGRIRQHP
RLCLQWHPRPPLADCGCTSNGIYYQLGSSFLTEDCSQRCTC
ASSRILLCEPP -> YAILCQBAGAALAGWRDRTLCAMBCP
                                                                                                                                                                                                                                                                                                                                                                                 HGVSSRYHISELYDTLPSILC -> YAILCQEAGAALAGWR
DRTLC (in isoform 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGVSSRYHISELYDTLESILCOPGRPRGLRGPLRGRIRQH
-> YAILCQEAGAALAGWRDRTLCAMECPAGTIYQSCMTPC
PASCANLADPGDCEGPCVEGCAD (in isoform 7).
                                                                                                                                                                                                                                                                                                                                                                                                                        -> YAILCOEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTIYQSCMTPCPASCANLADPGDCEGPCVEGCASIPGYAY
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FYTTd=vSP 001424.
Missing (in isoform 4).
/FTTd=VSP_001425.
                                                                                                                                                                                                                                                                  (POTENTIAL)
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2
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/FTId=VSP 001423.
HGVSSRYHISELYDTLPSILCQPGRPRG
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                                                                                                                                  ZONADHESIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
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Missing (In isoform 2).
/FTId=VSP_001429.
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BY SIMILARITY.
BY SIMILARITY.
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                                                  DGOCR -- YAILCOGRAGAALAGWRDRTLCANGCPAGTIYO
SCHTPCPAGACNIADPBOGGGCPCVBCGCASIPGTAYSGTOSL
PWLTVAAPAMASTTRSELAAGGGPGERAGGEPDGGWNWNVS
SWPFPFLAGGOLSD (in isoform 1).
FTICL-VSP 001430.
Missing (in isoform 1).
FTIGL-VSP_001431.
 HGVSSRYHISELYDTLPSILCQPGRPRGLRGPLRGRLRQHP
                    RLCLQWHPEPPLADCGCTSNGIYYQLGSSFLTEDCSQRCTC
                                 ASSRILLCEPFSCRAGEVCTLGNHTQGCFPESPCLQNPCQN
                                                                                                                                                                                                                                                                                                                        621 İPSEKPİLLİEKPTIP---SEKPTIPSEKPİ--SİEKPTVPTEEPİT-PİEBİTISMEB
                                                                                                                                                                                                                                                                                                                                                              77 PSKPTTK-----QRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK---P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 TINTTKTNITT-----TLLTNNTTGNPKLISOMETPHSISSEGNLSPSOVST----
                                                                                                                                                                                                                                                                                                                                                                                      "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
"Molecular cloning of human intestinal mucin (MUC2) cDNA.
Identification of the amino terminus and overall sequence similarity
to prepro-von Willebrand factor.";
J. Biol. Chem. 269:2440-2446(1994).
[2]
SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A.
MEDLINES-13158917, PubMed=1885763;
TOTIDARA N.W., Gum J.R., Jr., Culhane P.J., Lagace R.E., Hicks J.W.,
Petersen G.M., Kim Y.S.
                                                                                                                                                                               H -> Q (IN REF. 1, AAK01431/AAK01432/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Colon;
MEDLINE=93016075; PubMed=1400449;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.
Kim Y.S.;
                                                                                                                                                                                                                   ; Score 198.5; DB 1; Length 2812; Pred. No. 7.4e-06; 35; Mismatches 91; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         002817; 014878;
01-JUN-1994 (Rel. 29, Created)
01-NV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MUCIN 2 precursor (Intestinal mucin 2).
HOMO sapiens (Human).
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TOURCE FROM N.A.
TISSUB-Intestine;
MEDLINE-94132002; PubMed-8200571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
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                                                                                                                                                                                                                    16.2%;
                                                                                                                                                                                                                                       28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 ----TSEHPSQPSSPP
                                                                                                                                                                                                                                   Local Similarity 28.0 es 72; Conservative
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MUC2_HUMAN
ID _MUC2_HUMAN
                                                                                                                                           VARSPLIC
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         and polymorphism.;

1. Clim. Invest. 88:1005-1013(1991).

2. Clim. Invest. 88:1005-1013(1991).

3. Clim. Invest. 88:1005-1013(1991).

3. Clim. Invest. 88:1005-1013(1991).

4. Clim. Invest. 88:1005-1013(1991).

5. CATER WICHER WICHELE PUTHELIA OF THE INTESTINES, AIRWAYS, AND OTHER WICHS MUNCHARARS-CONTAINING ORGANS. THOUGHT TO PROVIDE A REGISTRY AIR WICHTERER.

5. CAGENTS AT WICHORALS.

5. CHORDINIT: MULTITURERIC.

6. SUBCELLULAR IOCATION: Secreted.

7. CHORDINIT: MULTITURERIC.

7. CHORDINIT: MULTITURERIC.

7. CHORDINIT: MULTITURERIC.

8. CHORDINIT: MULTITURERIC.

8. CHORDINIT: MULTITURERIC.

8. CHORDINIT: MULTITURERIC.

9. CHORDINITERED BONDS (BY SIMILARITY).

9. COATAINER MURBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLELS.

6. CHORDINITERIC CONTAINER IS CLEARING INhibitory-like) domain.

6. CHORDINITY: CONTAINER IN THE (TYPPSIN INhibitory-like) domain.
"MUC-2 human small intestinal mucin gene structure. Repeated arrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L21998; AAB95295.1; ---
EMBL; M7427; AAA59875.1; ---
EMBL; M94131; AAA59163.1; ---
EMBL; M94131; AAA59163.1; ---
EMBL; M94131; AAA59163.1; ---
EMBL; M94132; AA3932.
Genew; FGMC7.512; MUC2.
MIM; 158370; ---
GO; GO:0005803; C:8ecretory vesicle; TAS.
InterPro; IPR006209; Cyg Knot.
InterPro; IPR006209; EGF_like.
InterPro; IPR00209; TILCYSTICh.
InterPro; IPR001846; VWF_C.
InterPro; IPR001846; VWF_C.
Ffam; PF00009; VWC; 1.
Ffam; PF00093; VWC; 1.
FMART; SM00214; VWC; 2.
FMART; SM00214; VWC; 2.
FMART; SM00216; VWC; 2.
FMOSITE; PS00129; CTCK 2; 1.
FMOSITE; PS00129; CTCK 2; 1.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
FMOSITE; PS00129; VWFC_1; 2.
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Best Local Similarity 30.6%; Pred. No. 3.3e-05;
Matches 77; Conservative 23; Mismatches 114; Indels 38; Gaps
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                                                                                                                                         P. Subvance.

Y. TISSUE=Skin;

WEDLINE=93077556; PubMed=1447205;

A. Hauser F., Hoffmann W.;

RT C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic

RT G.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic

RT Dolymorphism.";

RL D. Biol. Chem. 267:24624(1992).

CC I. FUNCTION: Could be involved in defense against microbial infections. Protects the epithelia from external environment.

CC I. SUBCELLULAR LOCATION: Secreted.

CC I. ALTERNATIVE PRODUCTS:

CC COMMENTE Additional isoforms seem to exist. Experimental

CC Comment=Additional isoforms for some isoforms;
                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Integumentary mucin C.1 (FIM-C.1) (Fragment).
Xenopus laevis (African clawed frog).
Ekkaryota, Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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SMART; SMOOGS, PEREFOIL.

SMART; SMOOGS, PTREFOIL.

SMART; SMOOGS, PTREFOIL.

REPEAL; Glycoprotein; Alternative splicing.

NOW TER 1 144 8 X 8 AA APPROXIM
                          662 AA.
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                                                                                                                                                                                                                                                                                                                                       Name=4;
                                                                                                                                                                                                                                                                                                                                                                                             Name=7;
                                                                                                                                                                                                                                                                                                                    Name=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
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      RESULT 14
MUC1_XENLA
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84 QRQ-----NKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPT 137
                                                                                                                                                               348 LSQVADCKVEPSQRVDCGFRGITADQCRQKNCCFDSSISGTKW--CFYSTSQVAATKTTT 405
                                                                                                                                                                                                            135 KPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPŢINTTKTNITTLLINNTTGNPKLTS 194
                                                                                                                                                                                                                                     406 TPİTTTİ-PİTTTTİNPITTTİNPITTTİTTİTTKATTİTTTTTTTTKATT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 STSTTTTTRAPPTKPT-----CKSTSTTTTRAPPTGKTSTTTTT 119
240 KATPITITITKAIPITITITKAITITITP------TITITITIKAITIPITITI 287
                                                                            288 TPTTTTKATTTTTSGECKMEPSKREDCGYSGITESOCRTKGCCFDSSIPOTKWCFYT 347
                                                                                                                         93 -- PNNDFHFEVFNFVPCSI-----CSNNPTC------WAICKRIPNKKPGKKTTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 ISFSNLSEI-----TSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQT---QPSKPTTK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 IGFANVANCSDCGCPTKATTTCAPPTKPTCKSTSTTTTTTTTTTTTTTTTAPPTKPTCK 74
                                      61 QPTTVKTKNTTTTQT-----QPSKP-----TTKQRQNK-----PPNK---- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.9%; Score 183; DB 1; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.8e-06;
Matches 55; Conservative 10; Mismatches 68; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88332966; PubMed=3138416;
Martin C.H., Mayeda C.A., Mayerowitz E.M.;
"Evolution and expression of the Sgs-3 glue gene of Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila simulans (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCMI_TaxID=7240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 KKPTFKTTKKOLKPQTTKPKEVPT--TKPTEEPTINTTKTNITT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 HKPTTHSTPKTKPTKPTKPTKPTKHTTPKTKPTKHTTPTTT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 23 SALIVARY GLUE PROTEIN SGS-3.
24 217 SALIVARY GLUE PROTEIN SGS-3.
217 AA; 22750 MW; D29894E340257881 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Mol. Biol. 201:273-287(1988).
-! DEVELOPMENTAL STAGE: PRODUCED BY THIRD-INSTAR LARVAE.
PIR. S01358. S01358.
FlyBase: FBgn0012853; Dsim\Sgs3.
                                                                                                                                                                                                                                                                                               195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPRNTT 230
                                                                                                                                                                                                                                                                                                                     465 FTPT--TTTTPTTTTATTTT--PTTTTTTTT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 29, 2003, 17:38:38 Job time : 13.6943 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salivary glue protein Sgs-3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SGS3 DROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
SGS3_DROSI
                                                                                                                                                                                                                                                  g
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd. Copyright

OM protein - protein search, using sw model

October 29, 2003, 17:33:35; Search time 22.3245 Seconds (without alignments) 999.400 Million cell updates/sec Run on:

US-09-462-816-4 1229 1 HKVTLTTAIIQDATSQIKNT.....VSTTSEHPSQPSSPPNTTRQ 232

score: Perfect

Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB g Maximum DB g Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | ٠ | | | SUMMARIES | |
|--------|-------|-------|--------|---|-----------|--------------------|
| Result | | Query | | | | |
| No. | Score | Match | Length | 图 | a | Description |
| н | 1216 | 98.9 | | ч | MGNZRL | major surface glvc |
| 7 | 1120 | 91.1 | 298 | | MGNZ | major surface glvc |
| æ | 1052 | 85.6 | | N | JQ1208 | attachment protein |
| 4 | 1045 | 85.0 | | 7 | JQ1205 | attachment protein |
| Ŋ | 1042 | 84.8 | | ~ | JC5680 | |
| 9 | 1037 | 84.4 | | 7 | JQ1209 | t |
| 7 | 1033 | 84.1 | 297 | N | JQ1206 | |
| ω | 1019 | 82.9 | 298 | ~ | JQ1207 | |
| თ | 1009 | 82.1 | 297 | 7 | JQ1204 | |
| 10 | 505.5 | 41.1 | 292 | Н | MGNZ60 | - no |
| 11 | 497 | 40.4 | | ч | MGNZ18 | Burface |
| 12 | 425 | 34.6 | | ٦ | VHNZ | nucleocapsid profe |
| 13 | 202 | 16.4 | m | н | GSFF3 | salivary dine prot |
| 14 | 193 | 15.7 | 3020 | ~ | A43932 | mucin 2 precursor. |
| 15 | 191 | 15.5 | | N | A45155 | mucin FIM-C.1 - Af |
| 16 | 190 | 15.5 | 322 | 7 | A53715 | abomucin precureor |
| 17 | 188 | 15.3 | 1832 | ~ | T31113 | mucin-like glycopr |
| 18 | 186.5 | 15.2 | | ~ | T22696 | hypothetical profe |
| 19 | 185.5 | 15.1 | 379 | ~ | 850125 | larval glue protei |
| 20 | 183 | 14.9 | | ~ | 801358 | Balivary glue prot |
| 21 | 183 | | - | ~ | S57180 | probable membrane |
| 22 | 179 | 14.6 | | ~ | T46740 | microfilarial ghea |
| 23 | 178 | 14.5 | 250 | N | PQ0768 | U |
| 24 | 177 | 14.4 | | Н | MGNZBR | (0) |
| 25 | 175 | 14.2 | | 7 | T22808 | |
| 56 | 175 | 14.2 | | ~ | T29634 | |
| 27 | 172.5 | 14.0 | 327 | ~ | S20074 | |
| 78 | 171.5 | 14.0 | 216 | N | 151920 | |
| 67 | 170.5 | 13.9 | 263 | N | JQ2284 | |

| mucin SAC (clone J | glucan 1.4-alpha-q | Zonadhesin - nic | mucin, tracheal (A | hypotherical prote | promastigote surfa | רי פתט(ט) לעל היניונה | T71-7 protein - fr | galitrary glue anot | alvoorotein a . o | hymothetical prote | agoites sisloce | Glycoprofein G - b | STATE OF THE STATE | accacimment grycopi | hypothetical prote |
|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|-----------------------|--------------------|---------------------|-------------------|--------------------|-----------------|--------------------|--|---------------------|--------------------|
| \$53363 | S48478 | T34022 | A37232 | E86185 | \$20075 | S53362 | 862335 | 801360 | J02388 | T34369 | A53577 | P00769 | A48732 | A48292 | T34513 |
| 0 | Н | N | N | ~ | ~ | ~ | N | N | N | N | 2 | N | ~ | 10 | N |
| 279 | 1367 | 2476 | 294 | 402 | 371 | 477 | 393 | 263 | 263 | 1777 | 1630 | 248 | 263 | 1118 | 3507 |
| o. | æ. | 4. | ۳. | m. | ۳. | m. | ч. | 0 | 0 | 9 | 80 | ω. | - | 9 | ι. |
| 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 12 | 12 | 12 | 12 | 12 | 12.5 |
| 170.5 | 169.5 | 164.5 | 163.5 | 163.5 | 163 | 163 | 160.5 | 160 | 159.5 | 158 | 157.5 | 157 | 156.5 | 155 | 153.5 |
| 30 | 31 | 35 | 33 | 34 | 32 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

surface glycoprotein G - human respiratory syncytial virus (strain Long) major

Cispedies: human respiratory syncytial virus
Cispedies: human respiratory syncytial virus
Cispedies: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
Ciscoession: A32703; S12279
RiJohnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A; Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A; Reference number: A32703; MUID:87289657; PMID:2441388

A; Accession: A32703
A; Molecule type: mRNA
A; Residues: 1-298 < JOH>
A; Volecule type: mRNA
A; Residues: 1-298 < JOH>
A; Cross-references: GB:MI7212; NID:g333940; PIDN:AAA47411.1; PID:g333941
B; Garcia-Barreno.
B; Garcia-Barreno.
B; Bortela, A; Delgado, T.; Lopez, J.A.; Melero, J.A.
BREO J. 9, 4181-4187, 1990
A; Hille: Frame shift mutations as a novel mechanism for the generation of neutralizat: A; Reference number: S12279; MUID:91065351; PMID:2249671
A; Reference number: S12279
A; Molecule type: mRNA
A; Residues: 1-298 < GAR>
C; Mesidues: 1-298 < GAR>
C; Mesidues: 1-298 < GAR>
C; MeyWords: glycoprotein; transmembrane protein
B; 41-63/Domain: transmembrane #status predicted < TMN>
F; 85, 103, 135, 179, 237, 250, 251, 273, 294/Binding site: carbohydrate (Asm) (covalent) #stal

Gaps ö Query Match

98.9%; Score 1216; DB 1; Length 298;
Best Local Similarity 99.1%; Pred. No. 5.8e-75;
Matches 230; Conservative 0; Mismatches 2; Indels

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9 1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL ò 뭐

61 OPTIVKTKNITITOTOPSKPITKORONKPPNKPNNDFHPBVFNFVPCSICSNNPTCWAIC 120 ò 셤

KRIPNKKPGKKTTTKPTKKPTFKTTKKOLKPQTTKPKEVPTTKPTBEPTINTTKTNITT 180 181 셤 à

121

ò

246

LLINNITGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 232 247 ద

RESULT 2

MGNZ major surface glycoprotein G - human respiratory syncytial virus C;Species: human respiratory syncytial virus C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999

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C;Species: Human respiratory syncytial virus
C;Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 26-Feb-1998
C;Accession: JC5680
C;Accession: JC5680
X; Wang, Z; Qian, Y; Zhu, R; Deng, J; Du, J; Zhu, Z.
Chinese J. Virol. 12, 317-322, 1996
A;Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain is: A;Reference number: JC5680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Experimental source: strain B79
A.Force: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for res C.Superfamily: respiratory syncytial virus major surface glycoprotein G F;1-38/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il ildren and adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: human respiratory syncytial virus
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: J01205
S;Cane, Pa,; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: J01204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 OSTIVGIKNITITQAQPNKPITKQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPICWAIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEEPTINTTKTNITTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 KRIPNKKPGKRITIKPIKKPIPKITIKKGPKPOTIKSKEAPITIKPIEEPIINTIKINIITI 246
                                  61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFWFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                   121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTBEPTINTTKTNITT 180
                                                                                                                                                                                                                         187 KRIPNKKPGKKTTTKPTKKPTIKTTKKDLKPQTTKPKEVLITKPTEKPTINTTRINIETT 246
                                                                                                   127 QSTTVKTKNTTTTQIQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: respiratory syncytial virus major surface glycoprotein G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attachment protein - human respiratory syncytial virus (strain RSB1734) N;Alternate names: G protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LLTSNTTRNPELTSQMRTFHSTSSEGNPSPSQVSITSEYPSQPSGPBNTPR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LLINNITGNPKLISOMETFHSISSEGNLSPSOVSTISEHPSOPSSPPNITR 231
                                                                                                                                                                                                                                                                                                                                                                  181 LLINNTIGNPKLISOMETPHSISSEGNLSPSQVSTISEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.0%; Score 1045; DB 2; Length 297; 86.6%; Pred. No. 1.8e-63; ive 10; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,.-.ov,vomain: incraceilular #status predicted <INT>
F;39-66/Domain: transmembrane #status predicted <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein - Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-297 < CAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-298 <GEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC5680
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N.Alternate names: G protein
CiSpecies: human respiratory syncytial virus
CiSpecies: human respiratory syncytial virus
CiSpecies: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
CiAccession: J01208
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A A;Reference number: J01204; MuID:91374006; PMID:1895054
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C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                       C; Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il ildren and adults.
                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; GH
C,Accession: A94048; A93599; A04039
R;Wertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985
A;Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus A;Reference number: A94048; MUID:85216636; PMID:3858865
A;Accession: A94048
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C;Keywords: glycoprotein; transmembrane predicted <TNM>
F;88-66/Domain: transmembrane #status predicted <TNM>
F;88-66/Domain: transmembrane #status predicted
F;85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%; Score 1120; DB 1; Length 298; 92.7%; Pred. No. 1.6e-68; Live 5; Mismatches 12; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 92.7%
Matches 215; Conservative
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Best Local Similarity
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A; Residues: 1-297 < CAN>
                                                                                                                                                                                                                                                       A; Residues: 1-298 <WER>
                                                                                                                                                                                                                             A; Molecule type: mRNA
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Afacession: JQ1206
A;Molecule type: mRNA
A;Residues: 1-27 <CAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
ildren and adults.
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Reywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred
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A;Molecule type: mRNA
A;Residues: 1-298 «CANA
A;Note: the authors translated the codon ACC for residue 4 as Asn and AGC for residue C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract lidren and adults.
C;Comment: Respiratory syncytial virus major surface glycoprotein G
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status predi
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N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1207
R;Cane, P.A.; Matthew, D.A.; Pringle, C.R.
A;Gane, P.A.; Matthew, D.A.; Pringle, C.R.
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: JQ1204; MUID:91374005; PMID:1895054
A,Title: Identification of variable domains of the attachment (G) protein of subgroup A,Reference number: JQ1204, MUID:91374005, PMID:1895054
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                                                                                                                                                                                                                                                                                                                                                                                         Length 297;
                                                                                                                                                                                                                                                                                                                                                                                 84.1%; Score 1033; DB 2; Length 29
86.5%; Pred. No. 1.2e-62;
tive 5; Mismatches 26; Indels
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Best Local Similarity
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NiAlternate names: G protein
NiAlternate names: G protein
C;Species: human respiratory syncytial virus
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Peb-1997
C;Accession: JO1209
R;Cane, P.A.; Matthews; D.A.; Pringle, C.R.
J; Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A A;Title: Identification of variable physics of the prince number: JO1209
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
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A;Molecule type: mana adults
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
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F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
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N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1206
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                         Length 298;
                                                                      Query Match 84.8%; Score 1042; DB 2; Length 2
Best Local Similarity 86.6%; Pred. No. 2.9e-63;
Matches 201; Conservative 8; Mismatches 23; Indels
           F;67-298/Domain: extracellular #status predicted <BXC>
                                                                                                                                                                                                                                                                                                                                                           61
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major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: B32703
R;Johnson, P.R; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and 1A;Reference number: A32703; MUID:87289657; PMID:2441388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRIPNKKPGKKTTTKPTKKPTFKTT-KKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: human respiratory syncytial virus
Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
OPTIVKTKNTITIQIOPSKPTIKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
                             127 HHTTAQTKGRITTSTQTNKPSTKSRSKNPPKKPKDDYHFEVPRCSICGNNQLCKSIC
                                                                                                                                                   187 KTIPSNKPKKKPTIKPTNKPTTKTTNKRDPKTPAKMPKKEIITNPTKKPTLKTTERDTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 HKVTLITVIVQTIKNHTEKNISTYLTQVPPERVNSSKQPTTISPIHTNSATISPNTKSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
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A, Residues: 1-292 <JOH>
A, Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Keywords: glycoprotein; transmembrane protein
F;41-63/Domain: transmembrane #status predicted <TMN>
F;81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: human respiratory syncytial virus
CiDate: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-
CiDate: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-
CiAccession: A04026
RiBlango, N.; Venkatesan, S.
Nucleic Acids Res. 11, 5941-5951, 1983
A;Title: Amino acid sequence of respiratory syncytial virus capsid prot
A;Reference number: A04026
A;Reference number: A04026
A;References: A04026
A;Residues: 1-467 < ELBA
A;Residues: 1-467 < ELBA
A;Cross-references: GB:X00001; NID:g61215; PIDN:CAA24906.1; PID:g61216
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                                                                                                                                                                                                                                                       247 SQSTVIDITIPKYTIQQQSLHSTTSENTPSSTQIPTASE-PS-TSNP
                                                                                                                                                                                                                       180 TLLINNITGNPKLISOMETFHSISSEGNLSPSQVSTISEHPSQPSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 TLLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

40.4%; Score 497; DB 1;
Best Local Similarity 46.8%; Pred. No. 1.3e-26;
Matches 104; Conservative 28; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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C,Superfam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
MyAlternate names: attachment glycoprotein G
Sispeciaes: human respiratory syncytial virus
C;Speciaes: human respiratory syncytial virus
C;Speciaes: human respiratory syncytial virus
C;Accession: A3707
R;Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A;Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of A;Title: The respiratory syncytial virus subgroup by attachment glycoprotein: analysis of A;Reference number: A37077; MUID:90357765; PMID:1697126
A;Residues: 1-292 <SUL>
A;Residues: 1-292 <SUL>
A;Residues: 1-292 <SUL>
C;Genetics:
C;Genetics:
A;Gene: G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                               protein of subgroup
                                                                                                                                                                                                                                                                                                                                                                                                                         tract
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                                                                                                                                                                                                                                                                                                                                                                                                                   Comment: Respiratory syncytial virus commonly causes severe lower respiratory daren and adults.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 OPTIVKTKNITITOTOPSKPITKORONKPPNKPNNDFHFEVFNFVPCSICSNNPICWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEPTINTTKTNITT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                              Cispecies: human respiratory syncytial virus
Cibate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
Cibacession: JQ1204
RiCane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096; 1991
Airitle: Identification of variable domains of the attachment (G) protein or A; Reference number: JQ1204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 KRIPNKKPGKRTTTKPTKKPTLKTTKKDPKPQTTKSEEVPTTKLTEEPTINTTKTNITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
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                                                                         attachment protein - human respiratory syncytial virus (strain RSB642)
N;Alternate names: G protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: respiratory syncytial virus major surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LLTINITIGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSSPPNTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 PLTSNTARNPELISQMETFHSTSSEGNPSPSQVSITSEYPPQPSSPPNTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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47.6%; Pred. No. 3.5e-27;
tive 28; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.1%; Score 1009; DB 2
84.0%; Pred. No. 4.8e-61
ive 11; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.1%;
Best Local Similarity 84.0%;
Matches 194; Conservative 1
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Best Local Similarity 47.6
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-297 < CAN>
                                                                                                                                                                                                                                                                                                                                    A; Accession: JQ1204
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A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: '', 1925-1948, 'TTS', 1952-1954 «JAN»
A; Residues: '', 1925-1948, 'TTS', 1952-1954 «JAN»
A; Rxperimental source: bronchus
B; Xu, G; Huan, L; Khatri, I; Sajjan, U.S.; McCool, D; Wang, D; Jones, C.; Forstnation and Biochem Biophyse, Rese Commun. 183, 821-828, 1992
A; Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the CA; Reference number: PQ0328; MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Reaidues: 2037-3020 <GU3>
A; Reaidues: 2037-3020 <GU3>
A; Reaidues: 2037-3020 <GU3>
A; Reaidues: 2037-3020 <GU3>
A; Reperimental source: colon
A; Note: sequence extracted from NCBI backbone (NCBIP:116698)
A; Note: sequence extracted from NCBI backbone (NCBIP:116698)
A; Note: sequence extracted from NCBI backbone (NCBIP:116698)
A; Note: sequence extracted from NCBI backbone (NCBIP:116698)
A; Note: sequence extracted from NCBI backbone (NCBIP:116698)
A; Title: MCC-2 human small intestinal mucin gene structure. Repeated arrays and polyman annuber: A43932; MUID:91358717; PMID:1885763
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A; Residues: 1343-1350, L'.1352-1411,'S'.1413-1448,'P',1450-1503,'T'.1505-1915 <TOR>
A; Residues: 1343-1350, L'.1352-1411,'S'.1413-1448,'P',1450-1503,'T'.1505-1915 <TOR>
A; Crossreferences: GB:M74027; NID:g18863; FIDM:AAB59875.1; PID:g18864
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
B; Gun. J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, 1989
A; Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and evi-
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A,Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both up A,Raference number: A45106; MUID:93016075; PMID:1400449 A;Accession: A45106 A;Accession: A45106 A;Accession: A55106 A;Accession: A55106 A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession A;Accession 
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                                                                                                                                                                                           A;Molecule type: mRNA
A;Residuse: 656-1895 • GUI2>
A;Crosi-references: GB:M94131; NID:g186395; PIDN:AAA59163.1; PID:g186396
A;Note: sequence extracted from NCBI backbone (NCBIP:116706)
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F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
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15.7%; Score 193; DB 2; Length 3020;
Best Local Similarity 30.6%; Pred. No. 4.3e-05;
Matches 77; Conservative 23; Mismatches 114; Indels 3:
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A;Accession: A61257
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A,Residues: 2328-2342,'K',2344-2354 <XUG1>
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A; Residues: 2328-2468 < XUG>
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: 40329
R;Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.
A;Accession: 80329
R;Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.
A;Title: DBA sequences, gene regulation and modular protein evolution in the Drosophila
A;Reference number: 492904; MUID:83294545; PMID:6411930
A;Reference number: A92904; MUID:83294545; PMID:6411930
A;Residues: 1.307 cGRR>
A;Crose-references: GB:X01918; NID:g8581; PIDN:CAA25994.1; PID:g603989
C;Goment: This protein is produced by third-instar larvae.
A;Gene: sgs-3
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NyAlternate names: mucin SMUC-41
NyAlternate names: mucin SMUC-41
Syspecies: Home sapiens (man)
C;Dptes: Home sapiens (man)
C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text change 05-Nov-1999
C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number: A49963; MUID:94132002; PMID:8300571
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A/Residues: 1-639 <GUI>
A/Cross-references: GB:L21998
R/Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.B.; Kim, Y.S.
J. Biol. Chem. 267, 21375-21383, 1992
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                                                                                                                                                                                                          376 TLKTTKKDPKPQTTKSKEVPTTKPTEEPTINTTKTNIITTLLTSNTTGNPELLSQMETFH 435
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                                                            0; Gaps
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     90.2%; Pred. No. 1.5e-21;
tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                              201 STSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                                 436 STSSEGNPSPSQVSTTSEYPSQPSSPPNTPRQ 467
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C;Superfamily: salivary glue protein
C;Keywords: salivary gland; tandem repeat
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                                                       83; Conservative
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hes 77; Conserva
          Best Local Similarity
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R;Hauser, F.; Hoffmann, W.
J. Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1
A;Reference number: A45155; MUID:93077556; PMID:1447205
1564 PPPTTTTTPPPPTTTTPSPPTTTTTPPPPTTTTPSPPTTTTPPPTTTPPPTTTPSPPTT 1623
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                                                                                                                                                                                                                                                                                                                                      1676 PPITTPSS--PITTTPSPPTTTP--SSPITTTTPSSTTTPSSPPTTMTTP 1731
                                                                                                                                                                                                                                                                                 159 VPTTKPTEEPTINTTKTNITTTLLTNNTTGNPKLISQMETFHSTSSEGNLSPSQVSTTSE 218
                                                                                               99 FEVFNFVPCSICSNNPICWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKB 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 LSQVADCKVEPSQRVDCGFRGITADQCRQKNCCFDSSISGTKW--CFYSTSQVAATKTTT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 KAIPITITIKAIPITITIKAITITITP------TITITITKAITITITI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 TPTTTTTATTTTTTSGECKMEPSKREDCGYSGITESQCRTKGCCFDSSIPQTKWCFYT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 --PNNDFHFEVFNFVPCSI-----CSNNPTC-----WAICKRIPNKKPGKKTTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 KPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEBPTINTTKTNITTTLLTNNTTGNPKLTS 194
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15.5%; Score 191; DB 2; Length 662;
Best Local Similarity 29.0%; Pred. No. 1.2e-05;
Matches 80; Conservative 19; Mismatches 111; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 HPSQPSSPPNTT 230
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Search completed: October 29, 2003, 17:41:50 Job time: 23.3245 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 29, 2003, 17:41:00 ; Search time 40.7094 Seconds

(without alignments)
975.349 Million cell updates/sec
Title: US-09-462-816-4
Sequence: 1229-816-4
Sequence: 1 HKVTLTAIIQDATSQIKNT......VSTTSEHPSQPSSPPNTTRQ 232
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Sequence: 1 HKVTLHTAIIQDATSQIKNT......VSTTSEHPSQPSSEP Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 642050 seqs, 171146064 residues Total number of hits satisfying chosen parameters: 642050

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | ! | 9 | Ap | Ap | App | JQC | lďc | p] | Appl | App | ld. | ppj | ddt | ldc | ob] | Appl |
|---------------|--------------------------|--------------------|--------------------|--------------------|-------------------|---------------|----------|------------------|------------------|----------|----------|----------|----------|------------------|----------|------------------|
| | | 18, 4 | 1068, | 1068, | 108, 2 | ŧ, A <u>r</u> | 1, Ag | | | 74, 7 | | 42, Ag | 142, 7 | 50, Ag | | |
| | ផ្ត | 106 | | | | 9.14 | 9 | e 74, | | | e 44, | 9.42 | 9 14 | 5 | - | |
| | Description | Sequence 1068, | Seguence | Sequence | Seguence | Sequence | Seguence | Sequence | Sequence | Sequence | Seguence | Seguence | Sequence | Sequence | Sequence | Sequence |
| | , | | 68 | 68 | 8 | | | | | 4. | | | 2 | | | |
| | i | -106 | JS-09-833-263-1068 | IS-10-025-380-1068 | JS-09-801-368-108 | 7-14 | 7-84 | US-10-124-557-74 | US-10-124-557-58 | 7-10 | 7-44 | 7-42 | 7-14 | 7-50 | 7-46 | JS-10-124-557-60 |
| 24 | ; | -217 | 3-26 | 5-38 | 1-36 | 4-55 | 4-55 | 4-55 | 4-55 | 4-55 | 4-55 | 4-55 | 4-55 | 4-55 | 4-55 | 4-55 |
| CIT TANAMAN O | | -925 | 9-83 | 0-02 | 9-80 | 0-12 | 0-12 | 0 - 12 | 0-12 | 0-12 | 0-12 | 0-12 | 0-12 | 0-12 | 0-12 | 0-12 |
| i i | Ü. | US-09-922-217-1068 | ns-o | US-1 | US-0 | US-1 | US-1 | US-1 | US-1 | US-1 | US-1 | US-1 | US-1 | US-10-124-557-50 | US-1 | US-1 |
| |)B | 6 | 10 | 14 | 10 | 14 | 74 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 |
| | Query Match Length DB | 5179 | 5179 | 5179 | 1367 | 941 | 1022 | 1038 | 1049 | 1140 | 1270 | 1311 | 1313 | 1314 | 1320 | 1320 |
| de | Query Match | 15.7 | 15.7 | 15.7 | 13.8 | 13.2 | 13.2 | 13.2 | 13.2 | 13.2 | 13.2 | 13.2 | 13.2 | 13.2 | 13.2 | 13.2 |
| | Score | 193 | 193 | 193 | 169.5 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 | 162 |
| | Result No. | | 7 | ٣ | 4 | S | φ | 7 | æ | σ | 10 | 11 | 12 | 13 | 14 | 15 |

| 17, 200 | 4 4 4 4 4 4 | | 126, 126, 110, 488, 224, | Sequence 224, App Sequence 224, App Sequence 224, App Sequence 224, App Sequence 224, App Sequence 224, App Sequence 224, App Sequence 224, App |
|---|--|--|--|--|
| 14 US-10-124-557-48 14 US-10-124-557-40 14 US-10-124-557-52 14 US-10-124-557-2 14 US-10-124-557-62 9 US-09-216-393-341 | 12 US-09-216-393-344 12 US-10-321-856-341 12 US-10-321-856-341 12 US-10-029-386-32198 12 US-10-039-694-3 | 12 US-09-840-746-20 15 US-10-245-802-8 10 US-09-905-129-21 10 US-09-991-630-21 12 US-10-301-822-49 | 15 US-10-U3Z-1895-126 15 U3-10-176-847-54 15 US-10-177-293-110 11 US-09-984-130-48 12 US-09-36-353A-48 12 US-10-137-870-224 | 12 US-10-140-018-224 12 US-10-140-021-224 12 US-10-140-274-224 12 US-10-140-471-224 12 US-10-140-807-224 12 US-10-140-922-224 12 US-10-140-924-224 12 US-10-140-924-224 |
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ALIGNMENTS

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RESULT 1

19-922-217-1068

19-922-217-1068

Sequence 1068, Application US/09922217

Sequence 1068, Application US/09922217

GENERAL INFORMATION:
APPLICANT: Xu, diangentum
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Meagher, Madelaine Joy
APPLICANT: Mang, Tungtong
APPLICANT: Mang, Tungtong
APPLICANT: Mang, Yuqiu
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APPLICANT: Mang, Alith, Gardon E.
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 ----VKSNLQPTTVKTKNTTTT------OTQPSKPTTKQRQNKPPNKPNNDFH 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 VPTTKPTEEPTINTTKTNITTTLLTNNTTGNPKLTSQMRTFHSTSSEGNLSPSQVSTTSE
                                                                                                                                                                                                                                                                            APPLICANT: Carter, Darrick TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: COMPOUNDS FOR THEIR USE FILE REPERRICE: 210121.471214 CURRENT APPLICATION NUMBER: US/10/025,380 CURRENT FILING DATE: 2001-12-19 NUMBER OF SEQ ID NOS: 1129 SOFTWARE: FASTSEQ FOR Windows Version 4.0 SEQ ID NO 1068 LENGTH: 5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
15.7%; Score 193; DB 14; Length 5
Best Local Similarity 30.6%; Pred. No. 1.6e-06;
Matches 77; Conservative 23; Mismatches 114; Indels
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
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APPLICANT: Bushy, Robert
APPLICANT: Hecht, Peter
PPLICANT: Hecht, Peter
PPLICANT: Madden, Kevin
TICANT: Maxon, Mary
TOANT: Milne, Todd
TANT: No. US20020128250Alman, The
WT: Royer, John
T: Salama, Sofie
Sherman, Amir
Silva, Jeff
Silva, Jeff
Vurmerr
            Madeleine Joy
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                                                                                  Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
Wang, Aijun
     Meagher, Madelei
Stolk, John A.
Wang, Tongtong
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ORGANISM: Homo sapiens
US-10-025-380-1068
                                                                             APPLICANT:
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                                                                                                                                        1624 TPI--TPPTSTTLPPT----TTPSPPTTTTPPPPTTTPSPPTTTPSPPTTTP 1675
                                         1564 PPPTITITIPPPHTTTPSPPTTTTTPPPPTTTTPPPTTTTPPPTTTPPPTTTPSPPTT 1623
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                                                                                                                                                                                            159 VPTTKPTEEPTINTTKTNITTTLLINNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSE 218
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     -- QTQPSKPTTKQRQNKPPNKPNNDFH 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Wang, Aijun

APPLICANT: Clapper, Johathan D.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Meagler, Madeleine J.

TITLE OF INVENTION: DIAGNOSIS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

TITLE DEPERROR: 21011.471C12

CURRENT APPLICATION NUMBER: US/19/833,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARES FASESEQ for Windows Version 3.0

SEQ ID NO 1068

LENGTH: 5179
                                                                                               99 FEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1068, Application US/09833263
Patent No. US20020110547A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1068, Application US/10025380
Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
56 ----VKSNLQPTTVKTKNTTTT
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US-09-833-263-1068
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US-10-025-380-1068
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TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                               Length 1367;
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Sequence 14, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                        ; Score 169.5; DB 10; Length
; Pred. No. 2.7e-05;
36; Mismatches 94; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <university control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
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FILING DATE: 08-AUG-1989
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
LENGTH: 1367
                                                                                                                                                                                                                                                                                    ORGANISM: Saccharomyces cerevisiae
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STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.2%;
Matches 62; Conservative 3
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COMPUTER READABLE FORM:
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66 K------TKWTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.6%; Pred. No. 7e-05;
Matches 68; Conservative 26; Mismatches 104; Indels 7
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 KSAPTTPKEPAPTTİKSAPİTPKEPAPTİTKEPAPTTPKEP
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TELEPHONE: (617)876-1170
TELEPAK: (617)876-1170
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
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FILING DATE: 29-DEC-1989
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Sequence 84, Application US/10124557
// Publication No. US20020137894A1
// GENERAL INFORMATION:
// APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark, Stephen C.
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COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
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APPLICATION NUMBER: US 07/546,114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TKKPTFKTTK 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 APITIKSAPITIPKEPAPITIPKKPAPITIPKEPAPITIPKEPITIPKEPAPITKEPAPITIPK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                         78; Gaps
                                                                                                                                                                                                                                                                                                                                                         Query Match
13.2%; Score 162; DB 14; Length 1022;
Best Local Similarity 24.6%; Pred. No. 7.8e-05;
Matches 68; Conservative 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRY APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Genner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 TTKSAPTİPKE----PSPTTİKEPAPTTPKEPAPİT 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSRE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                  NAME: CSEIT, LUAIN
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: 31,822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-124-557-84
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             LENGTH: 1022 amino acids
                                                                                                                                           TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-10-124-557-74
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66 K-----TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 KDL-----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLINNTTGNPKLTS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TTAILODATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOUR: IBM PC compatible
COMPRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.2%; Score 162; DB 14;
Best Local Similarity 24.6%; Pred. No. 7.9e-05;
Matches 68; Conservative 26; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 OMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 TTKSAPTTPKE----PSPTTTKEPAPTTPKEPAPTT 438
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFRENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION:
(617)876-1170
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                  LENGTH: 1038 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
STATE: Massachusetts
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286

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 K-----TKNTTTTQTQPSKPTTKQRQNKPNKPNNDFHFEVFNFVPCSICSN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 NPTCWAICKRIPN-----KKPGKKTTTKP-------TKKPTFKTTK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 APTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 KDL-----KPOTTKPKGVPTTKP-----TEEPTINTTKTNITTLLTNNTTGNPKLTS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 104, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Track, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Genner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

COUNTER: 87 CambridgePark Drive
CITY: CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.2%; Score 162; DB 14; Length 10
24.6%; Pred. No. 8e-05;
tive 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 TIKSAPITPKE----PSPITIKEPAPITPKEPAPIT 481
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA: <Unknown>
PRIOR APPLICATION DATA: 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1899
ATTORNEY/AGENT INFORMATION:
NAME: CRETT, LUATH
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
FELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-124-557-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617)876-1170
TELEPRA: (617)876-5851
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1049 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 24.6% nes 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-124-557-104
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Matches
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372 KSAPTIPKEPAPTTİKSAPİTİPKEPAPTİTİKEPAPTIPKEP------APITIKEP 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 BPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKBPAPTTTKSAPTTTKEPAPT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 K-----TYNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNPVPCSICSN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 NPTCWAICKRIPN-----KKPGKKTTTKP-------TKKPTFKTTK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 APTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSRITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 13.2%; Score 162; DB 14; Length 1140; Local Similarity 24.6%; Pred. No. 8.9e-05; hes 68; Conservative 26; Mismatches 104; Indels 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Jacoba, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible
OPERALTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 TIKSAPITPKE ---PSPITIKEPAPITPKEPAPIT 572
                                                                                                    PRIOR DATE: 16-Apr-2002
CLASSIFICATION: CURLOND
PRIOR APPLICATION: CURLOND:
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 39-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELERAK: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION; SEQ ID NO: 104: US-10-124-557-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-124-557-44
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STATE: Massachusetts

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190 TSKVLAKPTPKAETTTK-----GPALTTPKEPTPTTPKEPASTTP---KEPTPTT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 K-----TKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 KSAPTIPKEPAPTITKSAPTIPKEPAPTITKEPAPTIPKEP------APTITKEP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TKKPTFKTTK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 APTTTKSAPTTPKEPAPTTPKKPAPTTPKBPAPTTPKEPTPTTPKEPAPTTKBPAPTTPK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTKSAPTTKEPAPT 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 TTALIODATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTPGVKSNLQPTTV
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13.2%; Score 162; DB 14; Length 1270;
Best Local Similarity 24.6%; Pred. No. 0.0001;
Matches 68; Conservative 26; Mismatches 104; Indels 78
                                                                                                                                                                                 COMPUTER: INDEPT COMPUTER: FLOURY COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUTER: INDEPT COMPUT
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-124-557-44
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                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 APTITKSAPITPKEPAPITPKKPAPITPKEPAPITPKEPIPTTPKEPAPITKEPAPITPK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 KDL-----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLINNTTGNPKLIS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 BPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP------APTTTKEP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.2%; Score 162; DB 14; Length 1311; 24.6%; Pred. No. 0.00011; tive 26; Mismatches 104; Indels 78
                                                                                                                                                                                                                                                  COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 NPTCWALCKRIPN-----KKPGKKTTTKP----
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 42: US-10-124-557-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 142, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                               ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)876-5851
                                                                                                       CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 42
SEQUENCE CHARACTERISTICS
NUMBER OF SEQUENCES: 143
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US-10-124-557-142
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US-10-124-557-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- APTITKEP 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 APITIKSAPITPKEPAPITPKKPAPITPKEPAPITPKEPITPTPKBPAPITKEPAPITPK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 KDL-----KPQTTKPKEVPTTKP-----TEBPTINTTKTNITTTLLINNTTGNPKLTS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TTALIQDATSQIKWTTPTYLTQDPQLGISFSNLSELTSQTTTLLASTTPGVKSNLQPTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.2%; Score 162; DB 14; Length 1313;
Best Local Similarity 24.6%; Pred. No. 0.00011;
Matches 68; Conservative 26; Mismatches 104; Indels 78
                                                                         OF INVENTION: Megakaryocyte Stimulating Factors OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                 CURRENT IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-DAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                          ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5190
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MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-124-557-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1313 amino acids
TYPE: amino acid
Stephen C.
                                    Hewick, Rodney M
Gesner, Thomas G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                               CITY: Cambridge
                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 02140
                                                                             Q
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RESULT

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66 K------TKNTTTTQTQPSKPTTKQRQNKPNKPNNDFHFEVFNFVPCSICSN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 ISKVLAKPTPKAETTTK-----GPALTTPKEPTPTTPKRPASTTP---KEPTPTT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 APTITKSAPITPKEPAPITPKKPAPITPKEPAPITPKEPIPITPKEPAPITKEPAPITPK 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 BPAPTAPKKPAPTTPKEPAPTTTKEPSPTTPKEPSPTTTKSPAPTTTKSPAPT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 KDL----KPQTTKPKEVPTTKP-----TEEPTINTTKTNITTLLINNTTGNPKLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTT1LASTTPGVKSNLQPTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TKKPTFKTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1314;
                                                                                                                                           Hewick, Rodney M.
Gesner, Thomas G.
IITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%; Score 162; DB 14; Length 1 24.6%; Pred. No. 0.00011; ive 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 NPTCWAICKRIPN-----KKPGKKTTTKP-
                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid

POPOLGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-124-557-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
Sequence 50, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                   APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                      Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617)876 - 5851
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.6'
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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397 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 456
                --TEEPTINTTKTNITTLLINNTTGNPKLTS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ISKVLAKPIPKABITIK------GPALTIPKEPİPTİPKEPASİTİP---KEPIPTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1320;
                                                                                                                                                                                                                             US-10-124-557-60
Sequence 60, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Gener, Thomas G.
TITLE OF INVENTION:
WUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 162; DB 14; Length 13
24.6%; Pred. No. 0.00011;
live 26; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                                                195 QMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                           457 TTKSAPTTPKE----PSPTTTKEPAPTTPKEPAPTT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Rloppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Ve-

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNV-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-124-557-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
         147 KDL----KPOTTKPKEVPTTKP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 60
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 24.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                               RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TKKPTFKTTK 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 TTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTLLASTTPGVKSNLQPTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READMER FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CONTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

CLASSIFICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

ATTORNEY/AGENT INFORMATION:
                                                                                                          US-10-124-557-46

Sequence 46, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP
451 TTKSAPTTPKE----PSPTTTKBPAPTTPKBPAPTT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 NPTCWAICKRIPN-----KKPGKKTTTKP-----
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617)876-1170
TELEPAR: (617)876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-124-557-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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Matches
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9

셤 ð 셤 ò

Search completed: October 29, 2003, 17:54:27 Job time : 41.7094 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2003, 17:36:05; Search time 12.6943 Seconds (without alignments) 773.267 Million cell updates/sec Run on:

US-09-462-816-4

1229 1 HKVTLTTAIIQDATSQIKNT.....VSTTSEHPSQPSSPPNTTRQ 232 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:* Database :

1: /cgr2_6/prodata/2/jaa/5A_COMB.pep:*
2: /cgr2_6/prodata/2/jaa/5B_COMB.pep:*
3: /cgr2_6/prodata/2/jaa/6A_COMB.pep:*
4: /cgr2_6/prodata/2/jaa/6B_COMB.pep:*
5: /cgr2_6/prodata/2/jaa/FCTUS_COMB.pep:*
6: /cgr2_6/prodata/2/jaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | | | | SUMMERTES | |
|---------------|-------|----------------|-----------|----|-------------------|-------------------|
| Result No. | Score | Query Match | Length DB | DB | αI | Description |
| н | 1229 | 100.0 | 298 | ~ | US-08-467-963C-8 | Sequence 8, Appli |
| 7 | 1229 | 100.0 | 298 | ~ | US-08-838-189D-8 | w |
| m | 1229 | 100.0 | 298 | ო | US-08-852-344D-8 | ₩ |
| 4 | 1229 | 100.0 | 298 | m | US-08-344-639E-8 | œ |
| S | 1229 | 100.0 | 298 | ო | US-08-467-969A-8 | w |
| 9 | 1229 | 100.0 | 298 | m | US-08-467-961A-8 | w |
| 7 | 1229 | 100.0 | 298 | m | US-08-001-554A-8 | Sequence 8, Appli |
| 89 | 901 | 73.3 | 681 | ø | 5194595-19 | |
| σ | 222 | 18.1 | 37 | ٣ | US-08-793-792-12 | Sequence 12, Appl |
| 10 | 193 | 15.7 | 32 | m | US-08-793-792-8 | 8, |
| 11 | 188 | 15.3 | 216 | m | US-08-928-361B-8 | œ, |
| 12 | 188 | 15.3 | 216 | 4 | US-09-588-995A-8 | æ |
| 13 | 188 | 15.3 | 1837 | m | US-08-928-361B-5 | 'n |
| 14 | 188 | 15.3 | 1837 | 4 | US-09-588-995A-5 | Sequence 5, Appli |
| 15 | 187.5 | 15.3 | 1721 | 'n | US-08-700-651-5 | 'n |
| 16 | 187.5 | 15.3 | | ო | US-08-928-361B-6 | ø |
| 17 | 187.5 | 15.3 | _ | 4 | US-09-588-995A-6 | ý |
| 18 | 181.5 | 14.8 | | m | US-08-928-361B-27 | 27 |
| 19 | 174 | 14.2 | | ~ | US-08-793-792-4 | 4 |
| 20 | 173.5 | 14.1 | 249 | m | US-08-700-651-15 | Sequence 15, Appl |
| 21 | 173.5 | | | m | US-08-928-361B-20 | 20 |
| 22 | 173.5 | | | 4 | US-09-588-995A-20 | 20 |
| 23 | 170.5 | | | S | PCT-US91-08177-13 | 13, |
| 24 | 164.5 | | | N | US-08-276-967-2 | લેં |
| 25 | 162 | | 941 | 4 | US-07-757-022B-14 | 14 |
| 26 | 162 | 13.2 | Н | 4 | US-07-757-022B-84 | 94 |
| 27 | 162 | | | 4 | US-07-757-022B-74 | 74, |
| | | | | | | |

| Sequence 58, Appl Sequence 104, App Sequence 44, Appl Sequence 42, Appl Sequence 50, Appl Sequence 60, Appl Sequence 60, Appl | Sequence 60, Appl Sequence 40, Appl Sequence 52, Appl Sequence 52, Appli Sequence 2, Appli | Sequence 62, Appl Sequence 341, Appl Sequence 12, Appl Sequence 12, Appl Sequence 17, Appl |
|---|--|---|
| US-07-757-022B-58 US-07-757-022B-104 US-07-757-022B-44 US-07-757-022B-42 US-07-757-022B-142 US-07-757-022B-46 | US-07-757-022B-60 US-07-757-022B-46 US-07-757-022B-40 US-07-757-022B-52 US-07-757-022B-2 | US-07-757-022B-62 US-09-216-393B-341 US-09-216-393B-344 US-08-700-651-12 US-08-928-361B-17 US-09-588-995A-17 |
| य य य य य य य य | **** | 4 4 4 6 6 6 4 |
| 1049 1270 1311 1311 1314 | 1354 1361 1363 1404 | 1404 288 288 175 175 |
| 23.25.25.25.25.25.25.25.25.25.25.25.25.25. | 13.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2 | 122.2 |
| 1622 | 162 162 162 162 | 162 161.5 161.5 158 158 |
| 8 9 0 H G G G | , w w w w | 44444 046640 |

ALIGNMENTS

```
GENERAL INFORMATION:

APPLICANT: KLEIN, Michel H
APPLICANT: KLEIN, Michel H
APPLICANT: ENASYSHYN, Mary E
APPLICANT: BUNASYSHYN, MARY E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038-474 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APPL-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-AN-1993
PRICE APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-AN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWARY, Michael 1
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-474 MI
               ; Sequence B, Application US/08467963C; Patent No. 5968776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-467-963C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                    Canada
                                                                                                                                                                                                                                                                                    ADDREAT: 64...
STREET: 64...
TW: Toronto
                                                                                                                                                                                                                                                                                                                                         CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: M5G 1R7
US-08-467-963C-8
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ö 67 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 126 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEBPTINTTKTNITT 180 ö 232; Conservative Matches

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121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 180
                                                                                          QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                           1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIFICATION AJS-
PRIOR APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9200117.1
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Pred. No. 3e-105;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 8, Application US/08467969A; Patent No. 6168786; GENEAL INFORMATION:
APPLICANT: Klain, Michel H; APPLICANT: Ewasyshyn, Mary E; TITLE OF INVENTION: Chimeric Immunogens; TUWERT OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Sci
100.0%; Pr
tive 0;
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH : 298 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity 100.(
Matches 232; Conservative
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STATE: Ontario
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QPITVKTKATITITQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                              KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 180
                                                                                                                                                                        187 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 246
                                                                QPITVKTKNTTTTQTQPSKPTTKQRQNKPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
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                                                                                                                                                                                                                                   LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFUNDA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: 14-NOV-1994
FLING DATE: 14-NOV-1994
CLASSIFICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
APPLICATION NUMBER: GB 9200117.1
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
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100.0%; Score 1229; DB 3;
Best Local Similarity 100.0%; Pred. No. 3e-105;
Matches 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08344639E
Patent No. 6033668
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/OCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEX: (65-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE GRARACTREISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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US-08-344-639E-8
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100.0%; Score 1229; DB 3
Best Local Similarity 100.0%; Pred. No. 3e-105;
Matches 232; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
SITY: Toronto
SIATE: Ontario
COUNTRY: Canada
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08001554A
Patent No. 6225091
GENERAL INFORMATION:
APPLICANT: Riein, Michel H
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/POCKET NUMBER: 1038-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELBERAK: (416) 595-1153
TELBERX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                            OPTIVKIKNITIIQIQPSKPITKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPICWAIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTIILASTTPGVKSNL 60
                                                                    QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
                                                                                                                                                                                     187 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEEPTINTTKTNITTT
                                                                                                                                                      KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
FILING DATE: 06-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
MED DATA NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
MED DATA NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
MED DATA NUMBER: 1038-476 MIS:bh
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100.0%; Score 1229; DB 3;
Best Local Similarity 100.0%; Pred. No. 3e-105;
Matches 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08467961A
Patent No. 6171783
GENERAL INFORMATION:
APPLICANT: Riein, Michel H
APPLICANT: Riein, Michel H
APPLICANT: Bwasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
INTHE OF INVENTION: Chimeric Immunogens
CORRESPONDENCE SIM & MCBUTHEY
ADDRESSEE: Sim & MCBUTHEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Sim & McBurney
330 University Avenue, 6TH Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RY: Canada
M5G 1R7
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186 180 246 ò 67 HKVTLTTALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTLLASTTPGVKSNL 126 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120 127 QPITVKIKNTITTQTQPSKPTTKQRQNKPPNKPNNDFHFBVFNFVPCSICSNNPTCWAIC KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 187 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEPTINTTKTNITTT KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT 1 HKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL Gaps LLTNNTIGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232 ö DB 3; Length 298; Indels COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993

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RESULT 10
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TITLE OF INVENTION: Antigenic peptides derived from the
TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: In Proppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610 KPQTIKSKEVPTIKPTEEPTINTIKINIITTLIISNITGNPELISQMETFHSISSEGNPS 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 QLGISPSNPSEITSQITTILASTIPGVKSTLÖSTTVKTKNTTTTĞTQPSKPTTKQRQNKP 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 QLGISFSNLSEITSQTTIILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                           247 LLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 298
181 LLINNITGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.3%; Score 901; DB 6; Length 681; Best Local Similarity 91.0%; Pred. No. 1.2e-74; Matches 172; Conservative 6; Mismatches 11; Indels
                                                                                                                          5194595-19
; PACENIC NO. 5194595
APPLICANT: WATHEN, MICHAEL W.
TITLE CANT: WATHEN, CHIMBRIC GLYCOPROTEINS CONTAINING
; INTELNO THE GLYCOPROTEINS OF HUMAN RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/543,780
FILING DATE: 31-0CT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 137,387
FILING DATE: 23-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence i2, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 37 amino acids
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; HYPOTHETICAL: NO
US-08-793-792-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 681
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Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
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TITLE OF INVENTION: PEPTIDES, POLYBEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MITANTS, VARLANTS, AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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                                                       Gaps
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Query Match
18.1%; Score 222; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.3e-14;
Matches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.7%; Score 193; DB 3; Length 32; 100.0%; Pred. No. 2.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                   91 NKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 127
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRERT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
                                                                                                                               1 NKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: PETERS, VERNY, JONES & BIKSA: 385 Sherman Avenue, Suite 6
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, 'CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/08928361B; Patent No. 6071518
                                                                                                                                                                                                                                                         Sequence 8, Application US/08793792; Patent No. 6077511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Conservative
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Anti
TITLE OF INVENTION: G-px
TITLE OF INVENTION: Of x
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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Matches 32; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94306-1840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
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| GENERAL INFORMATION: | APPLICANT: BERRATION: PETERSEN, CAROLYN
| APPLICANT: BERNES, DEBRA A. |
| APPLICANT: BRESON, ENCHAND C. |
| APPLICANT: BRESON, ENCHAND C. |
| APPLICANT: GTT, JIRI
| TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM |
| TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM |
| TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM |
| TITLE OF INVENTION: MERCHIONS |
| FILE REFERENCE: 480.19-5 |
| CURRENT APPLICATION NUMBER: 08/92, 361 |
| PRIOR FILING DATE: 1997-03-27 |
| PRIOR FILING DATE: 1997-09-12 |
| PRIOR APPLICATION NUMBER: 08/700, 651 |
| PRIOR APPLICATION NUMBER: 08/100, 651 |
| PRIOR APPLICATION NUMBER: 08/100, 651 |
| PRIOR PILING DATE: 1995-04-03 |
| NUMBER OF SEQ ID NOS: 115 |
| SEQ ID NO 8 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
15.3%; Score 188; DB 3; Length 216;
Best Local Similarity 26.4%; Pred. No. 8.3e-10;
Matches 60; Conservative 23; Mismatches 120; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 NNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
RESISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELEPHONE: 650-324-1677
TELEPHONE: 650-324-1677
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09588995A Patent No. 6514697
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12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-928-361B-8
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Sequence 5, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INPECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  64 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 123
                                                                                                                                                                                                                             124 PNKKPGKKTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTLLT 183
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                                                                                                                                       4 TLITALIODATSQIKNITPTYLIQDPQLGISFSNLSEITSQITTILASTIPGVKSNLQPT
                                                Gaps
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                                             24;
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                                                                                                                                                                                                                                                                                                                                                                       184 NNTTGNPKLISQMETFHSTSSEGNLSPSQVSTISEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                               172 TTTTTTTTTTTTTKRFTTT----TTTTTTTTKKFFTTTTTTTT 214
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  Length 216;
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15.3%; Score 188; DB 3; Length 183;
Best Local Similarity 26.4%; Pred. No. 1.4e-08;
Matches 60; Conservative 23; Mismatches 120; Indels
; Score 188; DB 4; Length 216; Pred. No. 8.3e-10; 23; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
ATYONRAY/ABARY INPORMATION:
NAME: Verly, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B: PETERS, VERNY, JONES & BIKSA
385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
ch 15.3%;
l Similarity 26.4%;
60; Conservative 2
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
Query Match
Best Local Similarity
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US-08-928-361B-5
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: PETERSEN, CAROLYN
APPLICANT: PARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
TITLE OF INVENTION: BICLAND FOR DETECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILER REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: 08/627,171
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO S: SEQ ID NOS: 115
SEQ ID NO S: SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID NOS: 113-15 SEQ ID 
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                                                                                                                                                                                                                                                                                                                    TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 123
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                                                                                                                                                                                                                                                                                                                                                                                                     184 NNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
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PATENT NO. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09588995A
Patent No. 6514697
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Matches 60; Conservative
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US-09-588-995A-5
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US-08-700-651-5
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APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPCOSPOCIDIUM PARVUM
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPCOSPOCIDIUM PARVUM
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT PILING DATE: 1997-08-14
ERRLIER APPLICATION NUMBER: 08/415,751
ERRLIER APPLICATION NUMBER: 08/415,751
ERRLIER PAPEL CATION NOS: 15
SOFTWARE: PACENTIN Ver: 2.0
SEQ 1D NO 5-
1-RNCTH-17-3-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTT------KPTEEPTINT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 TKTNITTILLTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%; Score 187.5; DB 3; Length 1721; 25.6%; Pred. No. 1.4e-08; tive 21; Mismatches 125; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October 29, 2003, 17:42:23 Job time : 13.6943 secs
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Conservative
APPLICANT: LEECH, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 61; Conserva
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 29, 2003, 17:11:05; Search time 52.966 Seconds (without alignments) 695.249 Million cell updates/sec

US-09-462-816-4 Perfect score:

1229 1 HKVTLTTAIIQDATSQIKNT.....VSTTSEHPSQPSSPPNTTRQ 232 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Amino acid sequenc RSV G protein pept RSV G protein pept Streptococcal prot Amino acid sequenc RSV subgp. A wil RSV subgp. A prote RSV Sub-group A wil RSV G protein anti A GZNa peptide der Amino acid sequenc | RSV subgroup A mod RSV subgroup A much RSV sub-group A mu Respiratory Syncyt RSV G protein anti Peptide which indu Amino acid sequenc Human G protein, G Peptide which indu Human G protein, G Peptide which indu Human G protein, G Peptide which indu Human G protein, G Amino acid sequenc RSV subgp. A prote Respiratory Syncyt RSV G protein anti Amino acid sequenc Human G protein anti Amino acid sequenc RSV G protein anti Amino acid sequenc RSV G protein anti Amino acid sequenc Human G protein anti Amino acid sequenc Human G protein anti Amino acid sequenc Human G protein |
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| 22 AAB67771 24 ABP97861 24 ABP97863 17 AAR9660 22 AAB66028 16 AAR86253 17 AAR96610 17 AAR96610 17 AAR96610 20 AAY4478 21 AAB1805 22 AAG67741 22 AAB64123 22 AAB67775 23 AAB67775 23 AAB67775 23 AAB67775 | 16 AAR8255 17 AAR95618 17 AAR95618 17 AAR95658 17 AAR97311 20 AAW97311 22 AA022581 23 AA022585 20 AAW97310 23 AA022585 24 AA022585 25 AAB68336 27 AAB68336 28 AA668336 29 AAB68336 20 AAR97063 20 AAR97063 20 AAR97063 21 AAR97063 22 AAB84135 |
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| 011241111111222222 | 7 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 |

ALIGNMENTS

AAW96314 standard; Protein; 232 AA. 28-JUN-1999 (first entry) AAW96314; RESULT 1 AAW96314

Secreted G protein of respiratory syncytial virus.

G protein; respiratory syncytial virus; RSV; recombinant vector; vaccine; immune response; immunogenicity; tPA; antibody; tissue plasminogen activator.

Respiratory syncytial virus.

WO9904010-A1

28-JAN-1999.

98WO-CA00697. 16-JUL-1998; 97US-0896442 18-JUL-1997; Klein MH, Li X, Sambhara S;

(CONN-) CONNAUGHT LAB LID.

WPI; 1999-132254/11. N-PSDB; AAX08422 Immunogenic composition for generating antibodies against

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTKTNITT 180
                                                                                               The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tpA). The recombinant vector may also comprise sequences upstream of the G protein gene which enhance the G protein generate antibodies directed against the RSV g protein when administered to a host organism. The composition is useful as a continuous of a palanced Th/Th2 immune response and for raising Ab, by usual immunisation and cell fusion methods. This truncated G protein is secreted since it lacks a transmembrane domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSRITSQTTTILASTTPGVKSNL
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIV; RSV; multimeric; hybrid; pathogen; chimeric protein; vaccine
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                                                                                                                                                                                                                                                                                                                                                                         Score 1229; DB 20; Length 232;
Pred. No. 3.6e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                     Claim 9; Fig 3; 67pp; English
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONN-) CONNAUGHT LAB
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ45686
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13-JAN-1994
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                                                                                                     A novel multimeric hybrid gene is used as a vaccine. The gene consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus (RsV)). The gene sequences that are particularly used are those which encode PIV-3 F and HN proteins (AAQ45683, AAQ45684) and RSV F and (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                            67 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                                                                                                                             QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein; respiratory syncytial virus; RSV; recombinant vector; vaccine; immune response; immunogenicity; tPA; antibody; tissue plasminogen activator.
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                                                                                                                                                                                                                                                                                    DB 14; Length 298;
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                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane bound G protein of respiratory syncytial virus.
           Multimeric hybrid genes and their chimeric proteins vaccines against multiple pathogenic infections e.g. para-influenza virus and respiratory syncytial virus
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                                                                                                                                                                                                                                                                                 100.0%; Score 1229; DB 14
100.0%; Pred. No. 4.7e-89;
tive 0; Mismatches 0;
                                                                            Claim 11; Figure 7A-7D; 80pp; English
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                                                                                                                                                                                                                                                     298 AA;
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                                                                                  The respiratory syncytial virus (RSV) G protein can be used in vaccines by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences immunoprotective ability. The resulting immunogenic composition will generate antibodies directed against the RSV G protein when administered to a host organism. The composition is useful as a vaccine to immunise against RSV-associated disease, particularly, by usual immunisation and cell fusion methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1229; DB 20; Length 298; 100.0%; Pred. No. 4.7e-89; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of human respiratory syncytial virus (HRSV) A2 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human respiratory syncytial virus (HRSV).
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to raise antibodies for diagnosis
                                             Claim 4; Fig 2; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            298 AA;
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61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNUPHFBVFNFVPCSICSNNPTCWAIC 120
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                                                                                                                A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV vaccines. The vaccine can be administered to pregnant women or women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                            91.1%; Score 1120; DB 8; Length 298; 92.7%; Pred. No. 1.8e-80; ive 5; Mismatches 12; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccines for human respiratory virus - include structural greeding for native structural viral proteins and immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human respiratory syncytial virus strain A2
                                                          Disclosure; Chart 13; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR25302 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86US-0818740.
88US-0218737.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 92.7
Matches 215; Conservative
syncytial virus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   major capsid protein; N.
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                                                                                                                                                                                                                                                                                                                                     298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ29623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-1986;
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                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR25302;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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vaccines against HRSV.

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                                                                                                                                                                                                                                                                         127 QSTTVKTKNITTTQTQPSKPTTKQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                           246
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                                                                                                                                                                                                             HKVTPTTAIIQDAISQIKNTTPTVLTQNPQLGISPSNPSEIISQITTILASITPGVKSTL
                                                                                                                                                                                                                                                                                                          KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITT
                                                                                                                                                                                                                                                                                                                                      KRIPNKKPGKKTTTKPTKKPTLKTTKKDPKPQTTKSKBVPTTKPTEPPTINTTKTNIITT
                                                                                                                                                                                    1 HKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSELTSQTTTILASTTPGVKSNL
AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer immunity against respiratory tract infections on human subjects. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of human respiratory syncytial virus glyco-protein F or (-by culturing eukaryotic host cells transfected with corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein G (ggs). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare
                                                                                                                                                                                                                                                                                                                                                                LLTNNTTGNPKLISQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                        91.1%; Score 1120; DB 13; Length 298; 92.7%; Pred. No. 1.8e-80; ive 5; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Columns 27-28; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW47605 standard; Protein; 298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHAA ) PHARMACIA & UPJOHN CO
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86US-0818740.
86WO-US02756.
92US-0897171.
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                                                                                                                                                       Matches 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-144802/13.
                                                                                                                         Query Match
Best Local Similarity
                                                                                           298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRSV glycoprotein
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                                                                                           Sequence
                                                                                                                                                                                                                  67
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                                                                                                                                                                    QSTIVKTKNTITICIQPSKPITKQRQNKPPSKPNNDFHFBVFNFVPCSICSNNPICWAIC 186
                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the inventors coid encoding a paramyxovirus (PMV) protein or its antigenic fragment. The virus may be administered in combination with an antivixal chemocherapeutic compound. Two or more viruses expressing different PMV proteins may be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PMV in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous nucleic acid
                                                                                                       RSV; G protein; heavily glycosylated protein; antianaemic; antiviral; vaccine; gene therapy; paramyxovirus; sendai virus; PMV; antiviral chemotherapetic compound; humoral response; cellular immune response; briV; paediatric respiratory disease; globin gene transfer; sickle cell disease; beta-thalassaemia; human immunodeficiency virus infection; HIV.
                                                                                      1 HKVTLITALIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                               KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTBEPTINTTKTNITT
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Sendai virus useful in vaccines to protect infection by paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment
                                                                                                                                                                                                                                                                                         LLTNNTTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSSPPNTTRQ 232
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                               298;
                               Length
                                                            Indels
                            Score 1120; DB 19;
Pred. No. 1.8e-80;
5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syncytial virus G protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                AAU74676 standard; Protein; 298
                           91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2001; 2001WO-US16610.
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                                                         Matches 215; Conservative
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                                           Similarity
298 AA;
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                                                                                                                                                                                                               121
Sequence
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                           Query Match
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                                            Local
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Chimeric polypeptide contg. a signal sequence and one or more immunogenic fragments from both human respiratory syncytial virus glycoproteins F and G. Can be used in vaccines. Hosts are, eg E. coli, Chinese hamster ovary cells, murine C127 cells and

frugiperda.

Claim 3; page 47-48; 50pp; English.

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encoding a second PMV protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral vector encoding a PMV protein. The recombinant virus is useful as an effective vaccine against helv or SBV (the major causes of paediatric respiratory disease) and also to express any gene of interest in target cells, providing a positive medical impact on impaired cells, Mild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathalssaemia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The Sendai virus replicates at level that is high enough to induce sufficient immunity, but does not cause any harm to human recipient. The present esquence represents a respiratory syncytial virus (RSV) G protein (heavily glycosylated protein), a PMV protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QPTTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRIPNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTEEPTINTTKTNITTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 KRIPNKKPGKKTTTKPTKKPTLKTTKKDPKPQTTKSKEVPTTKPTEEPTINTTKTNIITT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 HKVTPTTAIIQDATSQIKNTTPTYLTQNPQLGISPSNPSEITSQITTILASTTPGVKSTL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 QSTTVKTKNTTTTQTQPSKPTTKQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAIC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HKVTLTTAIIQDATSQIKNTTPTYLTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 LLTSNTTGNPELTSQMETFHSTSSEGNPSPSQVSTTSEYPSQPSSPNTPRQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric human respiratory synctial virus glycoproteins F and G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                 91.1%; Score 1120; DB 23; Length 298; 92.7%; Pred. No. 1.8e-80; ive 5; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric human respiratory syncytial virus polypeptides(s) - contg. immunogenic fragments from HRSV glycoproteins F and G, for vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric polypeptide; human respiratory syncytial virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP90441 standard; protein; 681 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein F; protein G; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 92.7
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                            298 AA;
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                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                      490 QLGISPSNPSEITSQITTILASTTPGVKSTLQSTTVKTKNTTTTQTQPSKPTTKQRQNKP 549
                                                                                                                                                                                                                                                                                      90 PNKPNNDFHPEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDL 149
                                                                                                                                                                                                                                                                                                                    550 PSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTLKTTKKDP 609
                                                                                                                                                                                                                                                                                                                                                  150 KPQTTKPKEVPTTKPTEEPTINTTKTNITTLLTNNTTGNPKLTSQMBTFHSTSSEGNLS 209
                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a fusion protein comprising a peptide derived from the G protein of Respiratory syncytial virus (RSV) linked to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria
                                                                                                                                                                                                                            30 QLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide derived from diphtheria anatoxin, useful as carrier in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSV G protein peptide G2Na and diphtheria anatoxin peptide DTb.
                                                                                                                                                                  Length 681;
                                                                                                                                                                                               11; Indels
                                                                                                                                                                73.3%; Score 901; DB 10; 91.0%; Pred. No. 8.6e-63; ive 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27-28; 42pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP97862 standard; protein; 361 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2001; 2001FR-0009733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium diphtheriae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                            Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              210 PSQVSTTSE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                             670 PSOVNISSO 678
                                                                                                                                                                               Similarity
                                                                                                                                    681 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR2827606-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP97862;
                                                                                                                                   Sequence
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                          124 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKBVPTTKPTEEPTIN------TTKT 175
                                                                                                                                                                                                                                                                             64 PNKKPGKKTTTKPTKKPTKKTTKKDHKPQTTKPE--GSINLDMDVIRDKTKT 120
                                                                                                                                                                                                                                  63
anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of Cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OmpA; P40; enterobacteria; nasal composition; respiratory tract; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract
                                                                                                                                                                                                                               4 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                    64 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                             Gaps
                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a fusion protein of P40 and RSV antigen.
                                                                                                                                                 Length 361;
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                  NITT------TLLTNNTTGNPKLTSQMETFHSTSSE 205
                                                                                                                                                                                                                                                                                                                                              121 KIESLKEHGPIKNKMSESPNKTVSEEKAKQYLEEFHOTALE
                                                                                                                                                                             50;
                                                                                                                                               DB 24;
                                                                                                                                            Score 580; DB 24
Pred, No. 8.3e-38
                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 31-32; 39pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB67771 standard; Protein; 452
                                                                                                                                           47.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-2000; 2000WO-FR02626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99FR-0011888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane protein A; RSV; RSV infection; lung;
                                                                                                                                                         Best Local Similarity 70.8
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kiebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goestch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-257929/26.
                                                                                                                 361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAFB0153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200121203-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corvaiea N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2001
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB67771;
                                                                                                                                                                                                                                                                                                                  176
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                      AAB6777
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                                                                                                                                                                                                                       430
                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a fusion protein comprising a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of cys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response
                                                                                                                                                   322 LAPDRRVEIEVKGYKEVVTQ-----PQGPG----DPMTVKTKNTTTTQTQPSKPTTKQ
                                                                                                                                                                                    85 RONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKT
                                                                                                                                                                                                     371 RQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKT
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide derived from diphtheria anatoxin, useful as carrier in vaccines, lacks at least one Cys residue, also related nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSV G protein peptide G2Na and diphtheria anatoxin peptide DTa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ons, or cancers and to generate, or increase, an immune infectious agents or tumour cells.
                                                                 Length 452;
                                                                                              Indels
                                                                                                                        25 LTQDPQLGISFSNLSEITSQTTTILASTTPGVKSNLQPTTVKTKNTT
 vaccines for prevention or treatment of RSV infections
                                                                DB 22;
                                                                                           18;
                                                             Score 572.5; DB 2
Pred. No. 4.2e-37;
                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 26-27; 42pp; French.
                                                                                                                                                                                                                                                 145 TKKOLKPOTTKPKEVPTTKPTE 166
                                                                                                                                                                                                                                                                 431 TKKDHKPQTTKPKEVPTTKPVD 452
                                                                                                                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                         ABP97861 standard; protein; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck A;
                                                              46.68;
76.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Respiratory syncytial virus
Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-2001; 2001FR-0009733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-2001; 2001FR-0009733
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                           Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nguyen NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-241969/25.
                                                                             Similarity
                              452 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR2827606-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                        ABP97861;
                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                against
                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                         ABP97861
SXS
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DB 24; Length 291;

45.9%; Score 564.5;

Query Match

The present sequence represents a fusion protein comprising a Klebsiella preumoniae outer membrane protein A (OmpA) designated P40 and a respiratory syncytial virus (R8V) antigen. Enterobacterium OmpA proteins, associated with an immunogenic peptide from R8V are used to prepare a nasal composition that induces a protective response, against R8V infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing

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                                                                                                                                                                                                                                                                                         64 PNKKPGKKTTTKPTKKPTKFKTTKKDHKPQTTKPKBVPTTKPGSGADDVVDSSKSFV---- 119
                                                                                                       64 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived from the Optotein of Respiratory syncytial virus (RSV) linked to a peptide derived from a diphtheria anatoxin. The diphtheria anatoxin peptide generates an immune response against any antigen coupled to it, and and has a negative, immediate hypersensitivity response. Diphtheria anatoxin derived peptides, when modified to lack at least one cysteine residue, are useful as carrier peptides. Deletion of tys residues in anatoxin peptides reduces formation of unwanted disulfide bridges. The peptides are used as a carrier for vaccines, particularly those for prevention or treatment of viral, bacterial, parasitic or fungal infections, or cancers and to generate, or increase, an immune response against infectious agents or tumour cells.
                                                                                                                                                                                                                                                    124 PNKKPGKKTTTKPTRKPTFKTTKKDLKPQTTKPKBVPTTKPTE--EPTINTTKTNITTL 181
                                                                                                                                                                             63
                                                                                                                                                4 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a fusion protein comprising a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide derived from diphtheria anatoxin, useful as carrier in vaccines, lacks at least one Cys residue, also related nucleic acids
                                    23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diphtheria anatoxin; immune response; antigen; carrier; G protein; hypersensitivity response; vaccine; infection; RSV; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSV G protein peptide G2Na and diphtheria anatoxin peptide DTaDTb
   Pred. No. 1.1e-36;
10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     182 LINNITGNPKLISQMETFHSISSEGNLSPSQVSTISEHPSQPSS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 29-30; 42pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP97863 standard; protein; 548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-2001; 2001FR-0009733.
67.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Respiratory syncytial virus.
Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2001; 2001FR-0009733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                    Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corvaia N, Nguyen NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-241969/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 AA;
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2827606-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP97863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP97863
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64 PNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKFGSGADDVVDSSKSFV--- 119
                               124 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKPTE--EPTINTTKTNITTL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence comprises a 219 amino acid fragment of streptococcal protein G, designated BB, fused to an immunogen, designated G2A, derived from amino acids 130-230 of protein G from Respiratory Syncytial Virus sub-group A or B. The BB fragment is able to bind to human serum albumin and thereby enhance immunogenicity of any antigen, hapten or immunogen that is covalently coupled to it. In this specific example, the BB fragment was found to induce T helper memory cells, leading to production of anti-G2A antibodies by stimulated
4 TVKTKUTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 63
                                                                                                                                                                                                                                                                                                                              Streptococcus; protein G; carrier protein; immunogenicity; increase; enhance; vaccine; anti-viral; human serum albumin; binding; immunostimulation; respiratory syncytial virus; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enhancing immunogenicity by coupling immunogen to serum albumin-binding protein - useful for preparing improved vaccines, e.g. against Respiratory Syncytial Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 562; DB 17; Length 349;
Pred. No. 2.1e-36;
                                                                                                                                                                                                                                                                                                    Streptococcal protein G fragment BB fused to RSV hapten G2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binz H, Nguyen Ngoc T, Nygren PA, Stahl S;
                                                                                            182 LTNNTTGNPKLTSQMETFHSTSSEGNLSPSQVSTTSEHPSQPSS 225
                                                                                                                         120 -------MENF---SYHGTKPGYVDSIQKGIQKPKS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247..347
/label= G2A
/note= "residues 130-230 of RSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...23
|label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 81-83; 102pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric Streptococcus sp.
Chimeric Respiratory Syncytial Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                        AAR95660 standard; Protein; 349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94FR-0013310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-FR01466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24..242
/label= BB
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-251766/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT31647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1995;
                                                                                                                                                                                                                                                                    21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9614416-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andreoni C,
                                                                                                                                                                                                                                      AAR95660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uhlen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                       AAR95660
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23; Gaps

DB 24; Length 548; 21; Indels

Query Match
Best Local Similarity 67.1%; Pred. No. 2.2e-36;
Matches 110; Conservative 10; Mismatches 21

64 TVKTKNTTTQTQPSKPTTKQRQNKPPNNDFHPEVFNFVPCSICSNNPTCWALCKRI 123

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us-09-462-816-4.rag

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                                                         272
                                                                                  PNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDL 149
                                                                                                                 332
                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes a method which uses quaternary aliphatic ammonium sales together with an immunogen or antigen to treat syncytial virus infections. The combination of the salt with the antigen or immunogen improves immunogenicity and equilibrates the Thl/Th2 immunogen improves immunogenicity and equilibrates the Thl/Th2 immunogenicity are response. The method is used for the treatment of respiratory syncytial comprising an albumin binding domain of the G protein of Streptococcus sp. tused to a G protein fragment of respiratory syncytial virus (VRS, leng version). The fusion protein is used as an antigen in the method
                                                                                                                                                                                                                                                                                                                                                      Aliphatic ammonium salt; immunogen; antigen; syncytial virus infection;
                                                                                                                                                                                                                                                                                                                          Amino acid sequence of fusion protein comprising 2 G protein fragments.
                                                                                                    37 NLSEITSQTTT--ILASTT-----PGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                             quaternary aliphatic ammonium salt and immunogen or antigen to respiratory syncytial virus infections
  10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
45.7%; Score 562; DB 22; Length 349;
Best Local Similarity 78.1%; Pred. No. 2.1e-36;
Matches 107; Conservative 10; Mismatches 10; Indels 10;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120..230
/note= "G protein fragment of VRS"
10;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                       AAB68028 standard; Protein; 349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 22-23; 35pp; French
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nguyen TN;
                                                                                                                                         150 KPQTTKPKEVPTTKPTE 166
                                                                                                                                                          333 KPQTTKPKEVPTTKPVD 349
                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99FR-0011284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99FR-0011284
                                                                                                                                                                                                                                                                                                                                                                     G protein; fusion protein.
                                                                                                                                                                                                                                                                                               (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beck A, Klinguer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-267782/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF84711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FR2798292-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-1999;
                                                                                                                                                                                                                                                                                                 29-JUN-2001
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                  9
                                                                                                                                                                                                                                                                     AAB68028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        combat
                                                                                                                                                                                                          RESULT 14
AAB68028
ID AAB68
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The sequence of the wild type amino acid residues 130-230 from the protein G of the respiratory syncytial virus (RSV) subgroups A. The sequence was used to synthesise the immunogenic peptides AAR88245-52 based on residues 174-187 of the subgroup A and B RSVs. The peptides are pref. conjugated to a novel carrier protein (the p40 protein; see AAR88257) derived from a membrane lipopolysaccharide (LPS) fraction from Klebsiella membrane LPSs with a divalent cation and detergents. Ribbiella membrane LPSs with a divalent cation and detergents, obtain an immunological adjuvant and linking the p40 protein to the above peptides. The conjugates are useful in the treatment of RSV A or B
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                273 PNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKFTFKTTKKOH 332
                                                                                                                                                                                                                                                                                                                                                                      Immunogenic peptide; protein G; respiratory syncytial virus; adjuvant; carrier protein; membrane lipopolysaccharide; LPS; Klebsiella pneumoniae; divalent cation; detergent; anion-exchange chromatography; infection.
                                                              PNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKKTTTKPTKKPTFKTTKKDL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 TVKTKNITITIQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
37 NLSEITSOTTT--ILASTT----PGVKSNLQPTTVKTKNTTTTQTQPSKPTTKQRQNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New respiratory syncytial virus polypeptide(s) for vaccine prodn. esp. by conjugation with new Klebsiella pneumoniae p40 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 558; DB 16; Length 101; Pred. No. 1e-36; 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                           RSV subgroup A wild type residues 130-230 (G2A clone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 PNKKPGKKTTTKPTKKPTFKTTKKDLKPQTTKPKEVPTTKP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thien NN, Trudel
                                                                                                                                                                                                                                             AAR88253 standard; peptide; 101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 23; 38pp; French.
                                                                                                                              KPQTTKPKEVPTTKPTE 166
                                                                                                                                                           333 KPOTTKPKEVPTTKPVD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94FR-0004009.
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                                                                                                                                                                                                                                                                                                             (first entry)
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baussant T, Binz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-353189/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FR2718452-A1
                                                                                                                                                                                                                                                                                                             15-MAY-1996
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                                                                                                                              150
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                                                                                                                                                                                                              RESULT 15
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Gaps

61 PNKKPGKKTTTKPTKKPTFKTTKKDHKPQTTKPKEVPTTKP 101

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